

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 6, 2006, 20:33:55 ; Search time 770 Seconds
(without alignments)
7621.839 Million cell updates/sec

Title: US-10-659-983A-18

Perfect score: 1467

Sequence: 1 ttgatcatggtcagattga.....acggcgagattcatgactgg 1467

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9267905 seqs, 2000278028 residues

Total number of hits satisfying chosen parameters: 18535810

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA New:*

- 1: /SIDSS/ptodata/2/pubpna/US08 NEW PUB.seq:*
- 2: /SIDSS/ptodata/2/pubpna/US06 NEW PUB.seq:*
- 3: /SIDSS/ptodata/2/pubpna/US07 NEW PUB.seq:*
- 4: /SIDSS/ptodata/2/pubpna/PCT_NEW PUB.seq:*
- 5: /SIDSS/ptodata/2/pubpna/US09 NEW PUB.seq:*
- 6: /SIDSS/ptodata/2/pubpna/US09 NEW PUB.seq1:*
- 7: /SIDSS/ptodata/2/pubpna/US10 NEW PUB.seq:*
- 8: /SIDSS/ptodata/2/pubpna/US10 NEW PUB.seq1:*
- 9: /SIDSS/ptodata/2/pubpna/US10 NEW PUB.seq2:*
- 10: /SIDSS/ptodata/2/pubpna/US10 NEW PUB.seq3:*
- 11: /SIDSS/ptodata/2/pubpna/US11 NEW PUB.seq:*
- 12: /SIDSS/ptodata/2/pubpna/US11 NEW PUB.seq2:*
- 13: /SIDSS/ptodata/2/pubpna/US11 NEW PUB.seq3:*
- 14: /SIDSS/ptodata/2/pubpna/US11 NEW PUB.seq4:*
- 15: /SIDSS/ptodata/2/pubpna/US60 NEW PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1133.4	77.3	1522	11 US-11-198-242-2	Sequence 2, Appli
2	1131.8	77.2	1526	11 US-11-198-242-1	Sequence 1, Appli
3	1067.6	72.8	1405	9 US-10-513-311-5	Sequence 5, Appli
4	1018.8	69.4	1501	9 US-10-513-639-1	Sequence 1, Appli
5	1009	68.8	1510	9 US-10-831-286A-48682	Sequence 48682, A
6	1007.4	68.7	1510	9 US-10-831-286A-48680	Sequence 48680, A
7	1006.6	68.6	1508	9 US-10-831-286A-48684	Sequence 48684, A
8	1006.6	68.6	1508	9 US-10-831-286A-48685	Sequence 48685, A
9	1006	68.6	1507	9 US-10-831-286A-48677	Sequence 48677, A
10	995.8	67.9	1530	9 US-10-831-286A-48671	Sequence 48671, A
11	988.8	67.4	1535	9 US-10-831-286A-48678	Sequence 48678, A
12	984	67.1	1494	9 US-10-831-286A-48691	Sequence 48691, A
13	983.8	67.1	1527	9 US-10-831-286A-48693	Sequence 48693, A
14	982.4	67.0	1493	9 US-10-831-286A-48683	Sequence 48683, A
15	979.2	66.7	1494	9 US-10-831-286A-48676	Sequence 48676, A
16	979	66.7	1519	9 US-10-831-286A-48687	Sequence 48687, A
17	978.2	66.7	1542	5 US-09-941-095-158	Sequence 158, App
18	978.2	66.7	1542	11 US-11-198-746-158	Sequence 158, App

19	978.2	66.7	1542	11 US-11-198-794-158	Sequence 158, App
20	978.2	66.7	1542	11 US-11-198-657-158	Sequence 158, App
c 21	977.2	66.6	1501	9 US-10-831-286A-48670	Sequence 48670, A
22	975.4	66.5	1495	9 US-10-831-286A-48675	Sequence 48675, A
23	974.8	66.4	1494	9 US-10-831-286A-48669	Sequence 48669, A
24	971	66.2	1503	9 US-10-831-286A-48665	Sequence 48665, A
c 25	970	66.1	1514	9 US-10-831-286A-48666	Sequence 48666, A
26	966.6	65.9	1533	9 US-10-831-286A-48668	Sequence 48668, A
c 27	964.4	65.7	1486	9 US-10-831-286A-48679	Sequence 48679, A
28	964	65.7	1492	9 US-10-831-286A-48686	Sequence 48686, A
29	956	65.2	1418	9 US-10-831-286A-48691	Sequence 48691, A
30	956	65.2	1418	9 US-10-831-286A-48692	Sequence 48692, A
c 31	955.8	65.2	1525	9 US-10-831-286A-48689	Sequence 48689, A
32	945.8	64.5	1481	9 US-10-831-286A-48672	Sequence 48672, A
c 33	944.4	64.4	1436	9 US-10-831-286A-48667	Sequence 48667, A
34	844.6	57.6	1485	14 US-11-055-637-76	Sequence 76, Appli
35	838	57.1	1545	14 US-11-055-637-66	Sequence 66, Appli
36	831.4	56.7	1587	11 US-11-273-617-8	Sequence 8, Appli
37	829.4	56.5	1510	11 US-11-273-617-9	Sequence 9, Appli
38	827	56.4	1521	14 US-11-151-847-1	Sequence 1, Appli
c 39	826.4	56.3	3657	8 US-10-793-626-4187	Sequence 4187, Ap
40	825.6	56.3	1509	11 US-11-273-617-6	Sequence 6, Appli
41	824.2	56.2	1535	14 US-11-055-637-74	Sequence 74, Appli
42	823.2	56.1	1555	5 US-09-941-095-160	Sequence 160, App
43	823.2	56.1	1555	11 US-11-198-746-160	Sequence 160, App
44	823.2	56.1	1555	11 US-11-198-794-160	Sequence 160, App
45	823.2	56.1	1555	11 US-11-198-657-160	Sequence 160, App

ALIGNMENTS

RESULT 1

US-11-198-242-2
; Sequence 2, Application US/11198242
; Publication No. US2006003545A1
; GENERAL INFORMATION:

; APPLICANT: AJINOMOTO CO., INC.

; TITLE OF INVENTION: Process for the production of beta-amino acids by using acylase

; FILE REFERENCE: AB04037

; CURRENT APPLICATION NUMBER: US/11/198,242

; CURRENT FILING DATE: 2005-08-08

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 2

; LENGTH: 1522

; TYPE: DNA

; ORGANISM: Burkholderia sp.

; FEATURE:

; NAME/KEY: 16S rDNA

; LOCATION: (1) ..(1522)

; OTHER INFORMATION:

; US-11-198-242-2

Query Match		77.3%;	Score 1133.4;	DB 11;	Length 1522;
Best Local Similarity		88.0%;	Pred. No. 0;		
Matches 1294;		Conservative	0;	Mismatches 166;	Indels 11; Gaps 5;
Qy	1	TTGATCATGGCTCAGATTGAACGCTGGCGGCGATGCTTTACACATGCAAGTGAACGGCAG	60		
Db	5	TTGATCTGGCTCAGATTGAACGCTGGCGGCGATGCTTTACACATGCAAGTGAACGGCAG	64		
Qy	61	CACGGGTCTTGACCTGGTGGCGAGTGGCGGAGTGGAGTAAATGATCGGAACGTGTC	120		
Db	65	CGCGGGGCGC--AACCTTGGCGCGGAGTGGCGGAACGGGTGAGTAATACATCGGAACGTGTC	122		
Qy	121	CAGAAGTGGGGGGAATAACGATCGAAAGATGTGCTAATACCGCATATTTCTTACCGAGGAA	180		
Db	123	CTGTAGTGGGGGGAATAGCCCGCGGAAGCCGGATTAAATACCGCATACGCTCTTACCGAGGAA	182		
Qy	181	AGCAGGGGATCGAAAGACCTTGTGCTTTTGGAGCGCGCATGCTGATTAGCTAGTTGGT	240		
Db	183	AGGGGGGATCTTAGGACCTCTCGCTACAGGGGGCGCGATGGCAGATGCTAGTTAGTTGGT	242		

QY 241 GGGTAAGGCTTACCAAGCAAGCATCAGTACTGTCTGAGAGGACGACGACAC 300
Db 243 GGGTAAGGCTTACCAAGGCGACGATCTGACTGTCTGAGAGGACGACGACAC 302
QY 301 TGGGACTGAGACACGCGCCAGACTCTCTACGGGAGGACGAGTGGGAAATTTTGGACAATG 360
Db 303 TGGGACTGAGACACGCGCCAGACTCTCTACGGGAGGACGAGTGGGAAATTTTGGACAATG 362
QY 361 GGGCAAGCTGATCAGCAATGCCGCTGAGTGAAGAGGC-TTCGGGTGTGAAGCTC 419
Db 363 GGGCAAGCTGATCAGCAATGCCGCTGAGTGAAGAGGCCTTCGGGTGTGAAGCAAC 422
QY 420 TTTTCAGTCGAGAAAGGTTGTGACTAATAATACAACTTATGATGGTACCGACAGAA 479
Db 423 TTTTGTCCGGAAAGAAACGCGGTGTTAATACCCGTGGCGGATGACGGTACCGGAAGAA 482
QY 480 GAAGCACCGGCTAACTACGTGCCAGCAGCGCGGTAAATACGTAGGGTGAAGGCTTAATC 539
Db 483 TAAGCACCGGCTAACTACGTGCCAGCAGCGCGGTAAATACGTAGGGTGAAGGCTTAATC 542
QY 540 GGAATTACTGGCGCTAAAGGTCGCGAGCGGCTTTGTAACTCAGATGTCAAATCCCAGG 599
Db 543 GGAATTACTGGCGCTAAAGGTCGCGAGCGGCTTCGCTTAAGCAGATGTGAATCCCAGG 602
QY 600 GCTTAACTGGCAATTCGTTTGAACCTACAAAGCTAGAGTGTAGCAGAGGGGGTGA 659
Db 603 GCTTAACTGGCAATTCGTTTGAACCTAGAGTGTAGCAGAGGGGGTGA 662
QY 660 TTCATGTGTAGCAGTGAATTCGCTAGAGATATCGAAGACATCGATGGCGAGGAGCC 719
Db 663 TTCACGCTGTAGCAGTGAATTCGCTAGAGATATCGAAGACATCGATGGCGAGGAGCC 722
QY 720 CCCTGGGTTTAACTGACGCTCATGCAAGAGCGTGGGAGCAACAGAGATTAGATACC 779
Db 723 CCCTGGGCAATATGACGCTCATGCAAGAGCGTGGGAGCAACAGAGATTAGATACC 782
QY 780 CTGTGTAGTCCAGCGCTTAAACGATGTCAACTGTGTGGGCTTTACTAGGCTTGGTAAC 839
Db 783 CTGTGTAGTCCAGCGCTTAAACGATGTCAACTGTGTGGGCTTTACTAGTAAAC 842
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QY 900 AATTGACGGGACCGCAAGCGGTGATTAATGTGGATTAAATTCGATGCAACCGCAAAA 959
Db 903 AATTGACGGGACCGCAAGCGGTGATTAATGTGGATTAAATTCGATGCAACCGCAAAA 962
QY 960 ACCTTACCTAACCTTGACATGTAGCGAATTTTAGAGATAAATAGTGCC--TTCCGGGA 1017
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Db 1023 GCATTAACAGAGTCTGATGGCTGTGCTAGCTGCTGCTGAGATGTTGGGTAAAGT 1082
QY 1078 CCGCAACGAGGCGCAACCCCTTGTCAATTAATGCCATCATTTAGTTGGGACCTTTAATGAG 1137
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QY 1318 GGAATCGCTAGTAAATCGCGGATCAGCATGTCCGGTGAATAGTTCCCGGCTTTGTACA 1377
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QY 1378 CACGCCCGCTCACACCATGAGGAGTGGTTTCCAGAGCAGAGATAGTCTAACCGTAA-GA 1436
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QY 1437 GGGCGTTTGGCCACGCGGAGATTCATGACTGG 1467
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RESULT 2
US-11-198-242-1
; Sequence 1, Application US/11198242
; Publication No. US20060035345A1
; GENERAL INFORMATION:
; APPLICANT: AJINOMOTO CO., INC.
; TITLE OF INVENTION: Process for the production of beta-amino acids by using acylase
; FILE REFERENCE: AB04037
; CURRENT APPLICATION NUMBER: US/11/198,242
; CURRENT FILING DATE: 2005-08-08
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1526
; TYPE: DNA
; ORGANISM: Variovorax sp.
; FEATURE:
; NAME/KEY: 16S rDNA
; LOCATION: (1)..(1526)
; OTHER INFORMATION:
US-11-198-242-1
Query Match 77.2%; Score 1131.8; DB 11; Length 1526;
Best Local Similarity 87.8%; Pred. No. 0;
Matches 1292; Conservative 0; Mismatches 172; Indels 7; Gaps 5;
QY 1 TTGATCATGCTCAGATTTCGAACGCTGGCGGCATGCTTTTACACATGCAAGTCCGAACCGCAG 60
Db 5 TTGATCATGCTCAGATTTCGAACGCTGGCGGCATGCTTTTACACATGCAAGTCCGAACCGCAG 64
QY 61 CACGGTGTCTTGACCTGGTGGCGAGTGGCGAGCGGTGAGTAATACATCGGAACGTGTC 120
Db 65 CCGGGGAGC--AATCTGGCGGCGAGTGGCGAAGCGGTGAGTAATACATCGGAACGTGTC 122
QY 121 CAGAAATGGGGATTAACGATCGAAGAGATGCTAATACCGCATATTTCTACGGAGGAA 180
Db 123 CAATCGTGGGGGATTAACGAGCGAAGAGCTGTGCTAATACCGCATACGATCTACGGATGA 182
QY 181 AGCAGGGGATTCGAAAGACCTTTGTGCTTTTGGAGCGGCGGATGCTGATTTAGCTAGTTGGT 240
Db 183 AGCAGGGGATTCGAAAGACCTTTGTGCTTTTGGAGCGGCGGATGCTGATTTAGCTAGTTGGT 242
QY 241 GGGGTAAAGGCTTACCAAGGCAACGATCAGTGTGTTGTTGAGAGGACGACGACAC 300
Db 243 GAGGTAAAGGCTTACCAAGGCTTTCGATCTGCTGAGAGGACGACGACGACAC 302
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QY 361 GGCAGAAAGCTGATTCAGCAATGCGCGTGAAGTGAAGAGG--CTTCGGGTGTGAAGCTC 419
Db 363 GGCAGAAAGCTGATTCAGCAATGCGCGTGAAGTGAAGAGG--CTTCGGGTGTGAAGCTC 422
QY 420 TTTTCAGTTCGAGAAAGAGGTTGTGACTAATAATCAACTTATGATGGTACCGACAGAA 479
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QY 480 GAAGCACCGGCTAATACGTCGACGAGCGCGGTAAATACGTAGGGTGAAGCGCTTAATC 539

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Qy 872 GTACGGTCGAGGATTAATAACTCAAGGAATTCAGCGGGACCCGCAACAGCGGTGGAATTA 931
Db 837 GTACGGCCGCAAGGTTGAACTCAAGGAATTCAGCGGGACCCGCAACAGCGGTGGAATTA 896
Qy 932 TGTGGATTAATTCGATGCAACGCGAAACCTTACCTACCTTTGACATGATGAGCAATATT 991
Db 897 TGTGGTTAATTCGATGCAACGCGAAACCTTACCTACCTTTGACATGATGAGCAATTCCT 956
Qy 992 TTAGAGATAAATAGTG--CCTTCGGGAAAGCTTAACACAGAGTGTGATGCTGCTGCTCA 1049
Db 957 TTAGAGATAGAGGAGTGCTCTGAAGAGAGCGGTAAACACAGGTGTGATGGCTGTGCTGCA 1016
Qy 1050 GCTCGTGTGAGATGTTGGGTTAAGTCCCGGAAAGAGCGCAACCTTGTCAATTAATTG 1109
Db 1017 GCTCGTGTGAGATGTTGGGTTAAGTCCCGGAAAGAGCGCAACCTTGTCAATTAATTG 1076
Qy 1110 CCATCATTTAGTGGGCACTTTAATGAGACTGCGGTTGACAAACCGGAGGAAGGTGGGA 1169
Db 1077 CTACGA-----AAGGGCACTTAATGGGACTGCGCGTGAACAAACCGGAGGAAGGTGGGA 1131
Qy 1170 TGAGCTCAAGTCTCATGGCCCTTATGGGTAGGCTTCACAGTAAATACAAATGCGCGTA 1229
Db 1132 TGAGCTCAAGTCTCATGGCCCTTATAGGTGGGCTACACACGTATACAAATGGCTGGTA 1191
Qy 1230 CAGAGGGTTGCAACCCGAGGGGAGCTAATCTCAGAAAGCGCGTCTGAGTCCGGATC 1289
Db 1192 CAGAGGGTTGCCAACCCGAGGGGAGCTAATCCCATAAAGCCAGTCTGAGTCCGGATC 1251
Qy 1290 GGAATCTGCAACTCGATCTCGTGAAGTGGGAAATCGCTAGTAATTCGCGGATCAGATGTCG 1349
Db 1252 GCATCTGCAACTCGATCTCGTGAAGTGGGAAATCGCTAGTAATTCGCGGATCAGAAATGCG 1311
Qy 1350 CGGTGAATACGTTCCCGGCTCTGTACACACCGCGCTGACACCATCGGAGTGGGTTTCA 1409
Db 1312 CGGTGAATACGTTCCCGGCTCTGTACACACCGCGCTGACACCATCGGAGTGGGTTTCA 1371
Qy 1410 CCAGAAGCAGATAGTCTAACCGTAAGAGGG 1439
Db 1372 CCAGAAGTAGGTAGCCTAACCGTAAGAGG 1401

RESULT 4
US-10-513-639-1
; Sequence 1, Application US/10513639
; Publication No. US20060010511A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Yicheng
; APPLICANT: Chen, Yancheng
; APPLICANT: Li, Fengmei
; APPLICANT: Tian, Zhexion
; APPLICANT: Lin, Min
; APPLICANT: Wang, Yiping
; TITLE OF INVENTION: NOVEL GLYPHOSATE-TOLERANT
; TITLE OF INVENTION: 5-ENOLPYRUVYLSHIKIMATE-3- PHOSPHATE SYNTHASE AND THE GENE
; FILE REFERENCE: 18495-002US1
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: CN 02117991.3
; PRIOR FILING DATE: 2002-05-28
; PRIOR APPLICATION NUMBER: CN 02117647.7
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: PCT/CN02/00539
; PRIOR FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Pseudomonas putida P.4G-1

US-10-513-639-1
Query Match 69.4%; Score 1018.8; DB 9; Length 1501;
Best Local Similarity 83.4%; Pred. No. 6.6e-304;
Matches 1228; Conservative 0; Mismatches 237; Indels 7; Gaps 6;
Qy 1 TTGATCATGGCTCAGATTGAACGCTGGGGGCAATGCTTTACATATGCAAGCTCGAACCGGAG 60
Db 6 TTGATCATGGCTCAGATTGAACGCTGGGGGCAATGCTTTACATATGCAAGCTCGAACCGG-AT 64
Qy 61 CACGGGTGCTTCACACCTGGTGGCGAGTGGCGGACGGGTGAGTAAATGTCATCGGAACGTGTC 120
Db 65 GAGAAGAGCTTCTCTTCGATTC-AGCGGCGAGCGGTGAGTAAATGCTTAGGAATCTGCC 123
Qy 121 CAGAAGTGGGGATTAACGCATCGAAAGATGTCTTAATACCGCATATCTCTACGGAGGAA 180
Db 124 TGTAGTGGGGGACAACTGTTTCGAAAGGAACGCTAATACCGCATAGCTCTACGGAGAA 183
Qy 181 AGCAGGGGATCGAAAGACCTTGTGCTTTTGGAGCGGCCGATGCTGATTAAGCTAGTTGGT 240
Db 184 AGCAGGGGACCTTTCGGGCCCTTGGGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGT 243
Qy 241 GGGGTAAAGGCTTACCAAGGCAACGATCAGTATGTTGGTCTGAGAGGACGACCAAGCCACAC 300
Db 244 GAGGTAATGGCTCACCAAGGCGACGATCCGTAATCTGCTGAGAGGATGATCAGTCACAC 303
Qy 301 TGGGACTGAGACACGCGCCAGACTCCTACGGGAGGAGCAGTGGGGAATTTTGGACAATG 360
Db 304 TGGAACTGAGACACGCGTCCAGACTCCTACGGGAGGAGCAGTGGGGAATTTTGGACAATG 363
Qy 361 GCGGAAGGCTGATCAGCAATGCCGCTGAGTGAAGAAAGG-CTTCGGGTGTGAAAGCTC 419
Db 364 GCGGAAGGCTGATCAGCAATGCCGCTGAGTGAAGAAAGGCTTCGGATTGTGAAAGCAC 423
Qy 420 TTTCACTCGAGAGAAAGGTTGTGACTAATATCAACTTATGATGTTGATCGACGAGAA 479
Db 424 TTTAAGTTGGGGAAGGGCAATTAACCTAATACGTTAGTGTGTTTGTGACGTTACCGACAGAA 483
Qy 480 GAGACACCGGCTAATCTACGTCAGGAGCGCGGTAAATACGTAGGCTGCAAGGCTTAATC 539
Db 484 TAAGCACCGGCTAATCTGTCGAGCGCGCGGTAAATACGTAGGCTGCAAGGCTTAATC 543
Qy 540 GGAATTAAGTGGGCTAAAGGGTGCAGAGCGGCTTTGTAAAGTCAAGTGTGAATATCCCGG 599
Db 544 GGAATTAAGTGGGCTAAAGCGCGGTAGGTGTTGTTAAAGTGTGAATATCCCGG 603
Qy 600 GCTTAACCTGGGAAATTCGTTGAAACTACAAGCTAGAGTGTAGCAGAGGGGCTGGAA 659
Db 604 GCTCAACCTGGGAACTGTATCCAAAGCTGGCAAGCTAGAGTACGGTAGAGGTTGGTGA 663
Qy 660 TTCCATGTGTAGCAGTGAATGCGTAGAGATATGGAAGAAACATCGATGGCGAAGGCGACC 719
Db 664 TTTCTGTGTAGCGGTGAATGCGTAGATATAGGAAGGAACACCAAGTGGCGAAGGCGACC 723
Qy 720 CCCTGGGTTAAACACTGACGCTCATGCAAGAAACGCTGGGGAGCAACAGAGTTAGATACC 779
Db 724 ACCTGGACTGATCTGACACTGAGAGTGCAGAAAGCGTGGGAGCAACAGAGTTAGATACC 783
Qy 780 CTGGTAGTCCAGCCCTTAACGATGTCACTAGTGTGTTGG-GCCTTACTAGGCTTGGTAA 838
Db 784 CTGGTAGTCCAGCCCGTAAACGATGTCACTAGCCGTTGGAATCCTTGAGATTTAGTGG 843
Qy 839 CGTAGCTTAACGCGTGAAGTTGACCGCTGGGAGTAGCGTCCGAGGATTAATAACTCAAG 898
Db 844 CGAGCTTAACGCATTAAGTTGACCGCTGGGAGTAGCGCGCAAGAGTTAAACTCAAT 903
Qy 899 GAATTGACGGGACCCGCAACAGCGGTGGAATTAATGCGATTAATTCGATCGAAGCGGAAA 958
Db 904 GAATTGACGGGCGCCGCAACAGCGGTGGAGCATGTGTTTAAATTCGAAAGCAAGCGGAAG 963
Qy 959 AACCTTACCTTACCTTGCATGTAGCGAAATATTTTAGAGATAAAATAGTGCCTTCGGGAA 1018
Db 964 AACCTTACCGGCTTGACATGACAGAACTTTCCAGAGATGGATTGTCCTTCGGGAA 1023


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Qy 1258 CTAATCTCAGAAAGCGCTGCTAGTCGGATCGAGTCTCGAACTCGACTCCGTGAAGTC 1317
Db 1261 CGGAACCTCATAAAGTGCCTGCTAGTCGGATTTGGAGTCTCGAACTCGACTCCATGAAGTC 1320
Qy 1318 GGAATCGCTAGTAATCCGCGATCAGCATGTCGGGTGAATACGTTCCCGGCTCTTGTAACA 1377
Db 1321 GGAATCGCTAGTAATCGTAGATCAGAACTGCTACGGTGNATACGTTCCCGGCTCTTGTAACA 1380
Qy 1378 CACGCCCGCTCACACCAATGGAGTGGGTTTCCACAGAAAGCAGATAGTCTAACCGT-AAAG 1436
Db 1381 CACGCCCGCTCACACCAATGGAGTGGGTTGCAAAAAGAGTAGGTAGCTTAAACCTTCGGGG 1440
Qy 1437 GGGCGTTTGGCAGCGCGAGATTCATGACTGG 1467
Db 1441 GGGCGCTTACCACCTTTGTGATTCATGACTGG 1471

RESULT 6
US-10-831-286A-48680
; Sequence 48680, Application US/10831286A
; Publication No. US20060046246A1
; GENERAL INFORMATION:
; APPLICANT: ZENG, QIANDONG
; APPLICANT: CHATELLIER, SONIA
; APPLICANT: MOIR, DONALD T.
; APPLICANT: LACROIX, BRUNA
; APPLICANT: CHILDRESS, DARRELL
; TITLE OF INVENTION: GENUS, GROUP, SPECIES AND/OR STRAIN SPECIFIC 16S rDNA SEQUENCES
; FILE REFERENCE: 032796-174.001
; CURRENT APPLICATION NUMBER: US/10/831.286A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/464,955
; PRIOR FILING DATE: 2003-04-24
; NUMBER OF SEQ ID NOS: 48788
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48680
; LENGTH: 1510
; TYPE: DNA
; ORGANISM: Moellerella wisconsinensis
US-10-831-286A-48680

Query Match 68.7%; Score 1007.4; DB 9; Length 1510;
Best Local Similarity 83.0%; Pred. No. 2.2e-300;
Matches 1221; Conservative 0; Mismatches 241; Indels 9; Gaps 6;

Qy 6 CATGGCTCAGATTGAACGCTGGCGCATGCTTTACACATGCAAGTCGAAACGCGACGACG- 64
Db 1 CATGGCTCAGATTGAACGCTGGCGCAGGCTTAACACATGCAAGTCGAGCGGTAAACAGGA 60
Qy 65 -GGTCTTGCNCC--TGGTGGCGAGTGGCGGACGGGTGAGTAAATGTCATCGGAAGCTGTC 121
Db 61 AGAAGCTTGTCTTCTTGTCTGACGAGCGCGGACGGGTGAGTAAATGATGGGATCTCGCT 120
Qy 122 AGAAGTGGGGATAACGCATCGAAAGATGTCTAATACCGCATATCTCTACGGAGGAAA 181
Db 121 GACAGAGGGGATAACTACTGGAAAACGGTAGCTAATACCGCATATCTCTAAGAGGCAAA 180
Qy 182 GCAGGGGATCGAAAGACCTTGTGCTTTTGGAGCGCGCGATGCTCGATAGTCTAGTGGTG 241
Db 181 GCAGGGGACCTTCGGGCTTGGCTGTGGATGAACCCATATGGATAGTAGTAGTGGTG 240
Qy 242 GGGTAAAGGCTTACAAAGGCAACCATCAGTAGTTGGTCTGAGGAGCGACGACCCACACT 301
Db 241 GGGTAAATGGGCTCACCTAGGCGACATCTTAGTGGTCTGAGAGGATGATCAGGCACACT 300
Qy 302 GGGACTGAGACACGGCCAGACTCTTACGGGAGGACGAGTGGGGAATTTTGGACAATGG 361
Db 301 GGGACTGAGACACGGCCAGACTCTTACGGGAGGACGAGTGGGGAATATTGCAATATGG 360
Qy 362 GCGAAAGCCTGATCAGCAATGCGCGGTGAGTGAAGAAGG-CTTCGGGTTGTAAAGCTCT 420
Db 361 GCGCAAGCCTGATGAGCCATGCGCGGTGATGAAGAAGGCTTTAGGGTTGTAAAGTACT 420
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Qy 421 TTCAGTCGAGAGAAAGAGTGTGTGACTAATAATCAAACTTATGATGGTACCACAGAAAG 480
Db 421 TTCAGTCGAGAGAAAGAGCGTGTGATATTAAATATCTATCAGCGATTGAGCTTACCACAGAAAG 480
Qy 481 AAGCACCGGCTAACTACGTGCGCAGAGCGCGGTAAATAGCTAGGGTGCAGCGTTTAATCG 540
Db 481 AAGCACCGGCTAACTCCGTGCGCAGAGCGCGGTAAATACGGGGGTGCAAGCGTTAATCG 540
Qy 541 GAATTAATCTGGCGGTAAAGGGTGCAGAGCGGCTTTGTAAAGTCAAGATGTGAAATCCCGGG 600
Db 541 GAATTAATCTGGCGGTAAAGCGCAGCGAGCGGCTTGATTAAGTTAGATGTGAAATCCCGGG 600
Qy 601 CTTAACTCTGGGATTTGGGTTTGAACCTACAAGCTAGAGTGTAGCAGAGGGGCTGGAAT 660
Db 601 CTTAACTCTGGGATGGCATCTTAAACTCGTCTAGAGTCTTTGTAGAGGGGGTGTAGAAAT 660
Qy 661 TCCATGTGTAGCAGTGAATTCGTGTAGAGATATGGAAGAAACATCGATGGCGAAGCGCACCC 720
Db 661 TCCATGTGTAGCGGTGAATTCGTGTAGAGATGTGGAGGAATACCGGTGGCGAAGCGCGCC 720
Qy 721 CTTGGGTTTAACTACGTACGCTCATGCAAGAAAGCGTGGGAGGCAACAGATTAGATACCC 780
Db 721 CTTGGAATAAAGACTGACGCTCAGGTGCGAAAGCGTGGGAGGCAACAGGATTAGATACCC 780
Qy 781 TGGTAGTCCACGCCCTAAACAGATGTC-AACTAGTTGTTGGGCTTACTAGGCTTGGTAAC 839
Db 781 TGGTAGTCCACGCTTAAACAGATGTCGATTTGAGAGTTGTTCCCTTGAGGAGTGGCTTCC 840
Qy 840 GTAGCTAAACCGGTGAAGTTGACCGCCTGGGGAGTACGGTGCAGAGATTAAAACTCAAAAG 899
Db 841 GGAGCTAAACCGGTTAAATCGACCGCCTGGGGAGTACGGCGCAAGGTTAAAACTCAAAATG 900
Qy 900 AATTGACGGGAGCCCGCACACAGGGTGGATTATGTCGATTAATTCGATCGAACCGCAAAA 959
Db 901 AATTGACGGGGCCCGCACCAAGCGGTGAGCATGTGTTTAAATTCGATCGAACCGCAAGA 960
Qy 960 ACCTTACCTACCTTCACATGATAGCAATATTTTAGAGATAAAATAGTGCCTTCGGGAAC 1019
Db 961 ACCTTACCTTCTTGCATTCAGAGAAATTTAGCAGAGATGCTTTAGTGCCTTCGGGAAC 1020
Qy 1020 GCTTAACACAGGTGCTGCATGGCTGTCGTGAGTCTGTCGTGAGATGTTGGGTAAAGTCC 1079
Db 1021 TCTGAGACAGGTGCTGCATGGCTGTCGTGAGTCTGTCGTGTTGTGAATGTTGGGTAAAGTCC 1080
Qy 1080 CGCAACGAGCGCAACCCCTTATCCTTTGTCGACGACGTTTAAATTCGATCGAACCGCAAGA 1137
Db 1081 CGCAACGAGCGCAACCCCTTATCCTTTGTCGACGACGTTTAAATTCGATCGAACCGCAAGA 1140
Qy 1138 ACTGCCGCTGACAAAACGGAGGAAGGTGGGGATGACGTCAAGTCTCATGGCCCTTATGG 1197
Db 1141 ACTGCCGCTGATAAACGGAGGAAGGTGGGGATGACGTCAAGTCTCATGGCCCTTACGA 1200
Qy 1198 GTAGGGCTTACACGTTAAATAAATGGCGGTACAGAGGGTTGCCAACCCCGAGGGGGAG 1257
Db 1201 GTAGGGCTACACGTTGCTACAAATGGCGCATACAAAGAGAAGCGAACTCCGAGAGCCAG 1260
Qy 1258 CTAAATCTCAGAAAGCGGTCGTAGTCGGGATCGAGTCTGCAACTCGACTCCGTGAAGTC 1317
Db 1261 CGAACTCTAAAGTGTGTCGTAGTCCGGATTCGGGATTCGAACTCCATGAAATGTC 1320
Qy 1318 GGAATCGCTAGTAATCGCGGATCAGCATGTGCGGGTGAATACGTTCCCGGGTCTTGTACA 1377
Db 1321 GGAATCGCTAGTAATCGTAGATCAGAAATGCTACGGTGAATACGTTCCCGGGCTTGTACA 1380
Qy 1378 CACGCCCGGTCAACCAATGGGAGTGGGTTTCCACAGAGCAGATAGTCTAACCGT-AAAG 1436
Db 1381 CACGCCCGGTCAACCAATGGGAGTGGGTTTCAAAAAGAGTAGGTAGCTTAAACCTTCGGGG 1440
Qy 1437 GGGCGTTTGGCCACGGCGAGATTTCATGACTGG 1467
Db 1441 GGGCGCTTACCACCTTTGTGATTCATGACTGG 1471
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RESULT 7
US-10-831-286A-48684
; Sequence 48684, Application US/10831286A
; Publication No. US20060046246A1
; GENERAL INFORMATION:
; APPLICANT: ZENG, QIANDONG
; APPLICANT: CHATELLIER, SONIA
; APPLICANT: MOIR, DONALD T.
; APPLICANT: LACROIX, BRUNA
; APPLICANT: CHILDRESS, DARRELL
; TITLE OF INVENTION: GENUS, GROUP, SPECIES AND/OR STRAIN SPECIFIC 16S rDNA SEQUENCES
; FILE REFERENCE: 032796-174.001
; CURRENT APPLICATION NUMBER: US/10/831,286A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/464,955
; PRIOR FILING DATE: 2003-04-24
; NUMBER OF SEQ ID NOS: 48788
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48684
; LENGTH: 1508
; TYPE: DNA
; ORGANISM: Providencia rustigianii
US-10-831-286A-48684

Query Match 68.6%; Score 1006.6; DB 9; Length 1508;
Best Local Similarity 82.6%; Pred. No. 3.9e-300;
Matches 1213; Conservative 0; Mismatches 249; Indels 7; Gaps 5;

Qy	6	CATGGCTCAGATTGAACCTGGCGCATGCTTTACACATGCAAGTCGAACCGCGACGCGG 65
Db	1	CATGGCTCAGATTGAACCTGGCGCGAGCGCTTAAACATGCAAGTCGAACCGGTAACAGG 60
Qy	66	G--TGCCTGCACTGGTGGCGAGTGGCGGAGGGGTGAGTATGATCGAAGCGTGTCCAG 123
Db	61	GAAGCTTCCTCTCGCTGACGAGCGCGGAGGGGTGAGTATGATGCGGATCTGCCCGA 120
Qy	124	AAGTGGGGGATAAAGCATCGAAAGATGTCTAATACCGCATATCTCTACGAGGAAAGC 183
Db	121	TAGAGGGGGATAAAGCATCGAAAGATGTCTAATACCGCATATCTCTTGGAGCAAGC 180
Qy	184	AGGGATCGAAGAACCTTGTGCTTTTGGAGCGCGCATGCTGATAGCTAGTGGTGGG 243
Db	181	AGGGAACTTCGGTCTTGGCTATCGGATCGGATGAACCCATATGGGATTAGCTAGTGGTGGG 240
Qy	244	GTAAGGCTACCAAGCAACGATCAGTATGCTCTGAGAGGACGACGACCACTGG 303
Db	241	GTAATGGTTCACCAAGGCGAGATCCCTAGCTGGTCTGAGAGGATGATCAGCCACACTGG 300
Qy	304	GACTGAGACACGGCCAGACTCCTACGGGAGCGAGCAGTGGGGAATTTTGGACAATGGGC 363
Db	301	GACTGAGACACGGCCAGACTCCTACGGGAGCGAGCAGTGGGGAATTTTGGACAATGGGC 360
Qy	364	GAAGCCTGATCCAGCAATCCGGTGTAGTGAAGAAGG--CTTCGGGTGTGAAGCTTTT 422
Db	361	GCAAGCCTGATCCAGCAATCCGGTGTATGAAGAAGGCCCTTAGGGTTGTAAAGTACTTT 420
Qy	423	CAGTCGAGAAAGAAAGTTGTGATTAATACAACTTATGATGTTACCCAGCAGAGAA 482
Db	421	CAGTTGGGAGAAAGCGTTGTATTAATATCATCAGCGATTTGACGTTTACCAACAGAGAA 480
Qy	483	GCACGGCTAATAGTCCAGCAGCGCGGTATATACGTAGGGTGCAGCGTTAATCGGA 542
Db	481	GCACGGCTAATAGTCCAGCAGCGCGGTATATACGTAGGGTGCAGCGTTAATCGGA 540
Qy	543	ATTACTGGCGTAAAGGGTGCAGAGCGGCTTTGTAGTCAGATGTGAAATCCCGGGCT 602
Db	541	ATTACTGGCGTAAAGCGACGCGAGCGGCTTTGTAGTAAAGTGTGAAATCCCGGGCT 600
Qy	603	TAACTGGGAATGGCTTTGAACTACAAAGCTAGATGTAGCAGAGGGGGGTGAATTC 662
Db	601	TAACTGGGAATGGCATCTAAGACTGTGGTCAGTCAGTGTCTTTGAGAGGGGGGTGAATTC 660
Qy	663	CATGTGTAGCAGTGAATGCGTAGAGATATGGAAGAACATCGATGGCGGAGCGACCC 722

Db	661	CATGTGTAGCGGTGAATGCGTAGAGATGTGGAGGAATACCGGTGCGGAGCGGCCCCC 720
Qy	723	TGGGTTAACTGACGCTCATGACGAAAGCGTGGGGAGCAAAACAGGATTAGATACCTTG 782
Db	721	TGGCAAAAGACTGACGCTCAGGTGCGAAAGCGTGGGGAGCAAAACAGGATTAGATACCTTG 780
Qy	783	GTAGTCCACGCGCTTAAACGATGTC--AACTAGTGTGTGGGCTTACTAGGCTTGGTAAAGT 841
Db	781	GTAGTCCACGCTTAAACGATGTCGATTTGAGGTTGTCTCTGAGAGTGGCTTCCGG 840
Qy	842	AGCTAAACGCGTGAAGTTGACCGCTTGGGGAGTACCGTGCAGGATTTAAACCTCAAAGGAA 901
Db	841	AGCTAAACGCGTGAAGTTGACCGCTTGGGGAGTACCGCGCAAGGTTAAACCTCAAATGAA 900
Qy	902	TTGACGGGACCCGACAGCGGTGATATATGTGATTAATTCGATGCAACGCGAAGAAC 961
Db	901	TTGACGGGACCCGACAGCGGTGATATATGTGATTAATTCGATGCAACGCGAAGAAC 960
Qy	962	CTTACCTACCTTCACATGTAGCGAATATTTTAGAGATAAAATAGTGCCTTCGGGAACGC 1021
Db	961	CTTACCTACTCTTGACATTCAGAGAAATTTAGCAGATGCTTTAGTGCCTTCGGGAATTC 1020
Qy	1022	TAAACAGGTGCTGCATGGCTGTCTGTCAGCTGTGTCTGAGATGTTTGGGTTAAGTCCCG 1081
Db	1021	TGACAGAGGTGCTGCATGGCTGTCTGTCAGCTGTGTGTGAAATGTTGCGTTAAGTCCCG 1080
Qy	1082	CAACGAGCGCAACCTTGTCTAATTTGCGCATCA--TTTAGTTGGGCACTTTAATGAGAC 1139
Db	1081	CAACGAGCGCAACCTTATCTTTTGTGCGACACGTCATGTTGGGAACTCAAAGGAGAC 1140
Qy	1140	TGCGGTGACAAAACCGGAGGAGGTGGGATGAGCTCAAGTCTCATGCGCCCTTATGGT 1199
Db	1141	TGCGGTGATATAACCGGAGGAGGTGGGATGAGCTCAAGTCTCATGCGCCCTTACGAGT 1200
Qy	1200	AGGCTTTCACACGTAATAACAATGGCGGTACAGAGGTTGCCAACCCCGAGGGGAGCT 1259
Db	1201	AGGCTACACACGTTGCTACATGGGTATACAAAGAGAAGCGCTCGCGAGAGCAAGG 1260
Qy	1260	AATCTCAGAAAGCGCGTGTAGTCCGGATCGGATCGGATCTGCAACTCGATCCGTTGAAGTCGG 1319
Db	1261	GAATCTATAAGTAGTACGTCGATCGGATTTGGAGTCTGCAACTCGACTCCATGAAGTCGG 1320
Qy	1320	AATCGCTAGTAATCCGCGATCAGCATGTCGCGGTGAATACGTTCCCGGCTCTGTACACA 1379
Db	1321	AATCGCTAGTAATCGTAGATCAGAAATGCTACGTTGAATACGTTCCCGGCTCTGTACACA 1380
Qy	1380	CCGCGCTTCACACCATGGGAGTGGGTTTTCACAGAGCAGATAGTCTAACCGT--AAGAGG 1438
Db	1381	CCGCGCTTCACACCATGGGAGTGGGTTTTCACAAAGAGATAGTCTAACCTTCGGGAGG 1440
Qy	1439	CGGTTTCCACGCGGAGATTTCATGACTGG 1467
Db	1441	CGGTTTACCACCTTTGTGATTTCATGACTGG 1469

RESULT 8

US-10-831-286A-48685
; Sequence 48685, Application US/10831286A
; Publication No. US20060046246A1
; GENERAL INFORMATION:
; APPLICANT: ZENG, QIANDONG
; APPLICANT: CHATELLIER, SONIA
; APPLICANT: MOIR, DONALD T.
; APPLICANT: LACROIX, BRUNA
; APPLICANT: CHILDRESS, DARRELL
; TITLE OF INVENTION: GENUS, GROUP, SPECIES AND/OR STRAIN SPECIFIC 16S rDNA SEQUENCES
; FILE REFERENCE: 032796-174.001
; CURRENT APPLICATION NUMBER: US/10/831,286A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/464,955
; PRIOR FILING DATE: 2003-04-24
; NUMBER OF SEQ ID NOS: 48788

```

; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48685
; LENGTH: 1508
; TYPE: DNA
; ORGANISM: Providencia rustigianii
US-10-831-286A-48685

Query Match      68.6%; Score 1006.6; DB 9; Length 1508;
Best Local Similarity 82.6%; Pred. No. 3.9e-300;
Matches 1213; Conservative 0; Mismatches 249; Indels 7; Gaps 5;

QY 6 CATGGCTCAGATTGAACGCTGGCGGATGCTTTTACACATGCAAGTCGAACGCGACGACGG 65
DB 1 CATGGCTCAGATTGAACGCTGGCGGAGCCCTTAAACATGCAAGTCGAGCGGTAAACAGGA 60

QY 66 G--TGCCTTGACCTGCTGGCGAGTGGCGAGCGGTCAGTAAATGCAATCGAACGTCGACG 123
DB 61 GAAGCTTTGCTTCGCTGACGAGCGCGGACCGGTCAGTAAATGTCATGGGATCTGCCCCGA 120

QY 124 AAGTGGGGGATACCGATCGAAGAATGTCTTAATACCGCATATCTCTACCGAGGAAAGC 183
DB 121 TAGAGGGGATTAAGTCTGGAACCGTACGTAATACCGCATATCTCTCAGGACGAAGC 180

QY 184 AGGGATTCGAAGACCTTGTCTTTTGGAGCGCGCGATGCCCTGATAGTCTAGTTGGTGG 243
DB 181 AGGGAACTTCGGTCTCTTGGCTATCCGATGAAACCCATATGGGATAGTCTAGTTGGTGG 240

QY 244 GTAAAGCCTTACCAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCGACCACTGG 303
DB 241 GTAAAGGCTTACCAAGGCGACGATCCCTAGTGGTCTGAGAGATGATAGCCCACTGG 300

QY 304 GACTGAGACACGCGCCCGACACTCTCTACGAGGAGCAGTCAGTGGGGAATTTTGGACAATGGC 363
DB 301 GACTGAGACACGCGCCCGACACTCTCTACGAGGAGCAGTCAGTGGGGAATTTTGGACAATGGC 360

QY 364 GAAAGCCTGATCAGCAATGCCGCTGAGTGAAGAAGG-CTTCGGGTTGTAAAGCTCTTT 422
DB 361 GCAAGCCTGATCAGCAATGCCGCTGAGTGAAGAAGGCTTTAGGGTTGTAAAGTACTTT 420

QY 423 CAGTTCGAGAGAAAAGGTTGTGACTAATAATCAACAATCTATGATGTTACCGACAGAGAA 482
DB 421 CAGTTGGAGAAAGGCTTGTGACTAATAATCGTCAACGATTCGATCTACCAACAGAGAA 480

QY 483 GCACCGGCTAACTACGTGCGCAGCAGCGCGGTAATACGTAGGGTGCAGCGTTAATCGGA 542
DB 481 GCACCGGCTAACTCCGTGCCAGCAGCGCGGTAATACGTAGGGTGCAGCGTTAATCGGA 540

QY 543 ATTACTGGCGGTAAGGCTGCGCAGCGCGCTTTTGTAAAGTCAGATGTGAAATCCCCGGCT 602
DB 541 ATTACTGGCGGTAAGGCTGCGCAGCGCGGTTGTTAAGTTAGTGTGAATCCCCGGCT 600

QY 603 TAACCTGGGAATTCGGTTTGAACACTACAAAGCTAGAGTGTAGCAGAGGGGGTGAATTC 662
DB 601 TAACCTGGGAATGTCATCTAAGACTGCTCAGCTAGAGTCTTGTAGAGGGGGGTAGAAATTC 660

QY 663 CATGTGTAGCAATGTAATGCTGAGATATGGAAGAACATCGATGCGGAGGAGCAGCCCC 722
DB 661 CATGTGTAGCGGTGAATATGCGTATGAGATGGAAGGAATACCGGTGGCGAAGGCGGCCCC 720

QY 723 TGGGTTAACTACTGACGCTCATGACAAAGCGTGGGGAGCAACAGGATTAGATACCCCTG 782
DB 721 TGGCAAAAGACTGACGCTCAGGTGCGAAGCGTGGGGAGCAACAGGATTAGATACCCCTG 780

QY 783 GTAGTCCACGCGCTTAAACGATGTC-AACTAGTTGTTGGGCTTATCTAGCGTTGGTAAAGT 841
DB 781 GTAGTCCACGCTGTAACAGATGTGCAATTTGGAAGTTGTTCCCTTTGAGGAGTGGCTTCGG 840

QY 842 AGCTAAACGCTGAGTTGACGCGCTGGGAGTACGTCGACGAGTTAAACACTCAAGAGAA 901
DB 841 AGCTAAACGCTGTAATGCAACGCTGGGAGTACGCGCGGAGGTTTAAACTTCAATGNA 900

QY 902 TTGACGGGGACCCGCCACAAGCGGTGGATTTATGGAATTAATTCGATGCAACCGGAAAC 961

```

Db 61 GAAGCTTCTCTCGCTGACGAGCGCGGATGAGTAATGTATGGGATCTGCCGA 120
 Qy 124 AAGTGGGGATTAACCATCGTAAAGATGTCTAATACCGCATATCTCTACGGAGGAAGC 183
 Db 121 TAGAGGGGATTAACCATCGTAAAGATGTCTAATACCGCATATCTCTAAGGAGGAAGC 180
 Qy 184 AGGGATCGAAAGACCTTGTGTCTTTTGGAGCGCGGATGCTCTAGTATAGTATAGTGGG 243
 Db 181 AGGGAACTTCGGTCTTTCGGCTATCGGATGAACCCATATGGATAGTATAGTGGG 240
 Qy 244 GTAAAGGCTACCAAGGCAACGATCAGATGTGTGTCTGAGAGGACGACACACATGG 303
 Db 241 GTAAAGGCTACCAAGGCAACGATCAGATGTGTGTCTGAGAGGATGATCAGACACATGG 300
 Qy 304 GACTGAGACACGGCCAGCATCTTACGGGAGGAGCAGTGGGGAATTTGGACATGGC 363
 Db 301 GACTGAGACACGGCCAGCATCTTACGGGAGGAGCAGTGGGGAATTTGGACATGGC 360
 Qy 364 GAAAGCCTGATCCAGCAATGCCGTGATGAAGAAGG-CTTCCGGTTGTAAAGCTCTTT 422
 Db 361 GCAAGCCTGATCGACCATGCCGTGTATGAAGAAGGCCCTAGGGTTGTAAAGTACTTT 420
 Qy 423 CAGTCGAGAAAGAGTTGTGAATAATAACAACCTTATGATGTGATACCGACAGAA 482
 Db 421 CAGTCGAGAAAGAGTTGTGAATAATAACAACCTTATGATGTGATACCGACAGAA 480
 Qy 483 GCACGGCTACTAGTCCAGCAGCGCGGTGATACCTGAGTGCAGCGTAAATCGGA 542
 Db 481 GCAACGGCTACTAGTCCAGCAGCGCGGTGATACCTGAGTGCAGCGTAAATCGGA 540
 Qy 543 ATTACTGGCGTAAAGGTCGCGAGCGCGCTTTGTAAGTCAGATGTGAAATCCCGGCT 602
 Db 541 ATTACTGGCGTAAAGGTCGCGAGCGCGCTTTGTAAGTCAGATGTGAAATCCCGGCT 600
 Qy 603 TAACTGGGAATGCGTTTGAACCTAACAAGTACGATGTGAGAGGGGGTGAATTC 662
 Db 601 TAACTGGGAATGCGTTTGAACCTAACAAGTACGATGTGAGAGGGGGTGAATTC 660
 Qy 663 CATGTGTAGCAGTGAATGCGTACGATGTGAGAGAACTGAGTGCAGCGAGCGCC 722
 Db 661 CATGTGTAGCAGTGAATGCGTACGATGTGAGAGAACTGAGTGCAGCGAGCGCC 720
 Qy 723 TGGGTTAACTGACGCTCATGACGAAAGCGTGGGAGCAAAAGAGTATGATACCTG 782
 Db 721 TGGACAAAGATGACGCTCATGAGTGGGAGCAAAAGAGTATGATACCTG 780
 Qy 783 GTAGTCCACGCTTAAACGATGTC- AACTAGTGTGTGGGCTTACTAGGTTGGTAAAGT 841
 Db 781 GTAGTCCACGCTTAAACGATGTC- AACTAGTGTGTGGGCTTACTAGGTTGGTAAAGT 840
 Qy 842 AGCTAAACGCTGAAAGTTCAGCGCTGGGAGTACGGTGCAGGATTAACCTCAAGAA 901
 Db 841 AGCTAAACGCTGAAAGTTCAGCGCTGGGAGTACGGTGCAGGATTAACCTCAAGAA 900
 Qy 902 TTGACGGGACCGCACAAGCGGTGATGATGATTAATTCAGTCAACGCAAGAAAC 961
 Db 901 TTGACGGGACCGCACAAGCGGTGATGATGATTAATTCAGTCAACGCAAGAAAC 960
 Qy 962 CTTAACCTTACCTGACATGTAGCGAATATTTAGAGATTAATAATAGTCTTCGGGAACG 1021
 Db 961 CTTAACCTTACCTGACATGTAGCGAATATTTAGAGATTAATAATAGTCTTCGGGAACG 1020
 Qy 1022 TAAACAGGTCGATGCTGCTGTCAGCTCGTGTGATGATGTTGGGTTAAGTCCG 1081
 Db 1021 TGAACAGGTCGATGCTGCTGTCAGCTCGTGTGATGATGTTGGGTTAAGTCCG 1080
 Qy 1082 CAACAGGTCGATGCTGCTGTCAGCTCGTGTGATGATGTTGGGTTAAGTCCG 1140
 Db 1081 CAACAGGTCGATGCTGCTGTCAGCTCGTGTGATGATGTTGGGTTAAGTCCG 1140
 Qy 1141 GCCGGTGAACAAACGGAGGAGGTGGGATGACGTCAAGTCAATCATGCGCCCTTACGAGTA 1200
 Db 1141 GCCGGTGAACAAACGGAGGAGGTGGGATGACGTCAAGTCAATCATGCGCCCTTACGAGTA 1200

Qy 1201 GGGCTTACACGTAATCAATGGCGGCTACAGAGGTTGCCAACCGCGAGGGGAGCTA 1260
 Db 1201 GGGCTTACACGTAATCAATGGCGGCTACAGAGGTTGCCAACCGCGAGGGGAGCTA 1260
 Qy 1261 ATCTCAGAAAGCGGTCGTAGTCCGGATCGGAGTCTGCAACTCTGACTCCCGTGAAGTCGA 1320
 Db 1261 AACTCATAAAGTACGTCGTAGTCCGGATCGGATTCGACTCTGACTCCATGAAGTCGA 1320
 Qy 1321 ATCGTAGTAATCGGGATCAGCATGTCGGGTGAATACGTTCCCGGCTCTTGTACAC 1380
 Db 1321 ATCGTAGTAATCGTAGATCAGAAATGCTACGTTGAATACGTTCCCGGCTCTTGTACAC 1380
 Qy 1381 CGCCGTCACACCACTGGGAGTGGGTTTCCACAGAGCAGATAGTCTAACCGT-AAAGAGG 1439
 Db 1381 CGCCGTCACACCACTGGGAGTGGGTTTCCACAGAGCAGATAGTCTAACCGT-AAAGAGG 1440
 Qy 1440 CGTTTCCACGCGGAGATTCATGCTG 1467
 Db 1441 CGTTTACCACCTTTGTGATTCATGCTG 1468

RESULT 10

US-10-831-286A-48671
 ; Sequence 48671, Application US/10831286A
 ; Publication No. US20060046246A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ZENG, QIANDONG
 ; APPLICANT: CHATELLIER, SONIA
 ; APPLICANT: MOIR, DONALD T.
 ; APPLICANT: LACROIX, BRUNA
 ; APPLICANT: CHILDRESS, DARRELL
 ; TITLE OF INVENTION: GENUS, GROUP, SPECIES AND/OR STRAIN SPECIFIC 16S rDNA SEQUENCES
 ; FILE REFERENCE: 032796-174.001
 ; CURRENT APPLICATION NUMBER: US/10/831.286A
 ; CURRENT FILING DATE: 2004-04-26
 ; PRIOR APPLICATION NUMBER: 60/464,955
 ; PRIOR FILING DATE: 2003-04-24
 ; NUMBER OF SEQ ID NOS: 48788
 ; SOFTWARE: Patent in version 3.2
 ; SEQ ID NO 48671
 ; LENGTH: 1530
 ; TYPE: DNA
 ; ORGANISM: Citrobacter youngae
 US-10-831-286A-48671

Query Match 67.9%; Score 995.8; DB 9; Length 1530;
 Best Local Similarity 82.4%; Pred. No. 8.5e-297;
 Matches 1215; Conservative 0; Mismatches 252; Indels 8; Gaps 6;

Qy 1 TTGATCATGGCTCAGATTGAACGCTGGCGGATGCTTTTACACATGCAAGTCGAACGGCAG 60
 Db 7 TTGATCATGGCTCAGATTGAACGCTGGCGGATGCTTTTACACATGCAAGTCGAACGGTAG 66
 Qy 61 CAC--GGTGTCTTCACT--GGTGGCAGTGGCGACGGGTGAGTAAATGATCGAACG 116
 Db 67 CACAGAGAGCTTCTCTCTGGGTGACGAGTGGCGACGGGTGAGTAAATGCTGGAAC 126
 Qy 117 TGTCCAGAGTGGGGATAACGATCCGAAAGATGTCTTAATACCGCATATTTCTCTACGA 176
 Db 127 TGCCCGATGGAGGGGATAACCTACTGGAAACGGTAGCTAATACCGCATAAAGTTCGAAGA 186
 Qy 177 GGAAGCAGGGATCGAAAGACCTTGTCTTTGGAGCGCGGATGCTCTGATGATAGT 236
 Db 187 CCAAGAGGGGGAGCTTCTGGGCTCTTGGCATCGGATGTCCTGATGGGATAGTAGT 246
 Qy 237 TGTGGGCTTAAAGGCTTACCAAGGCAACGATGAGTGTGTCTGAGAGGACGACCGC 296
 Db 247 AGTGGGGTAAAGGCTTACCTAGCGGACGATCCCTAGCTGTCTGAGAGGATGACCGC 306
 Qy 297 AACTGGGATGAGACACGCGCCAGATCTCTTAACGGAGGACGAGTGGGGAATTTGGAC 356
 Db 307 AACTGGAACTGAGACACGCGTCCAGATCTCTTAACGGAGGACGAGTGGGGAATTTGGAC 366

QY	357	AATGGCGAAGCCTGATCCAGCAATCCGCGTGAAGAGG-CTTCGGGTTGTAAA	415	QY	1433	AAGAGGGCGTTGCCACGGCGAGATTTCATGACTG3	1467
Db				Db			
QY	367	AATGGCGCAGCCTGATGAGCCATGCGCGTGTATGAAGAGGCCCTTCGGGTTGTAAA	426	QY	1447	GGAGGGCGCTTACCACTTTGTGATTTCATGACTG3	1481
Db				Db			
QY	416	GCTCTTTTCACTCGAGAGAAAAGGTTGTGACTAATTAATCAAACTTATGATGTGACGAC	475	QY			
Db				Db			
QY	476	AGAAGAGCACCCTTAACCTACTGTCAGCAGCCGCGTAAATACGTAAGGTGCAAGCGTT	535	QY			
Db				Db			
QY	487	AGAAGAGCACCCTTAACCTACTGTCAGCAGCCGCGTAAATACGTAAGGTGCAAGCGTT	546	QY			
Db				Db			
QY	536	AATCGGAATTAACCTGGGCGTAAAGGGTGCAGCGCGCTTTGTAAGTCAGATGTGAATATC	595	QY			
Db				Db			
QY	547	AATCGGAATTAACCTGGGCGTAAAGGGTGCAGCGCGCTTTGTAAGTCAGATGTGAATATC	606	QY			
Db				Db			
QY	596	CGGGCTTAACCTGGGAAATTCGTTTGAACCTAACAAGCTAGAGTGTAGCAGAGGGGGGT	655	QY			
Db				Db			
QY	607	CGGGCTTAACCTGGGAAATTCGTTTGAACCTAACAAGCTAGAGTGTAGCAGAGGGGGGT	666	QY			
Db				Db			
QY	656	GGAATTCATGTGTAGCAGTGAATGCTAGAGATATGGAAGAACATCGATGCGAAGGC	715	QY			
Db				Db			
QY	667	AGAATTCAGGTGTAGCGGTGAATGCTAGAGATCTGGAGGAATACCGGTGGGAAGGC	726	QY			
Db				Db			
QY	716	AGCCCCCTGGGTTAACTGACGCTCATGCAAGAGCGTGGGAGCAACAGGATTAGA	775	QY			
Db				Db			
QY	727	GGCCCCCTGGGTTAACTGACGCTCATGCAAGAGCGTGGGAGCAACAGGATTAGA	786	QY			
Db				Db			
QY	776	TACCTCGTAGTCCACCGCTTAACGATGTCAC- TAGTTGTTGGGCTTTACTAGGCTTG	834	QY			
Db				Db			
QY	787	TACCTCGTAGTCCACCGCTTAACGATGTCAC- TAGTTGTTGGGCTTTACTAGGCTTG	846	QY			
Db				Db			
QY	835	GTAACGTAGCTAAACCGTGAAGTTGACCGCTGGGGAGTAGCGTTCGAGAGTTAAATCTC	894	QY			
Db				Db			
QY	847	CTTCGGGAGCTAAACCGTGAAGTTGACCGCTGGGGAGTAGCGTTCGAGAGTTAAATCTC	906	QY			
Db				Db			
QY	895	AAAGGAATGTACGGGAGCCGCAACAGCGTGGATTAATGAGATTAATCGATGCAACGC	954	QY			
Db				Db			
QY	907	AAATGAATGTACGGGAGCCGCAACAGCGTGGAGCATGTGTTTAATCGATGCAACGC	966	QY			
Db				Db			
QY	955	GAAACCTTACCTACCTTACATGTAGCAATATTTAGAGATAAAATAGTCCCTTCG	1014	QY			
Db				Db			
QY	967	GAAGAACCTTACCTTACTCTTGACATCCAGAGAACTTAGCAGAGATGCTTTGGTCCCTTCG	1026	QY			
Db				Db			
QY	1015	GGAACGTAAACACAGGTGCTGATGCTGTCGTCAGTCTGTCGTGATGATGTTGGTTA	1074	QY			
Db				Db			
QY	1027	GGAACCTGAGACAGGTGCTGATGCTGTCGTCAGTCTGTCGTGATGATGTTGGTTA	1086	QY			
Db				Db			
QY	1075	AGTCCCGCAACGAGCGCAACCTTGTCAATTAATGCCATC-ATTAGTTGGGCACTTTAA	1133	QY			
Db				Db			
QY	1087	AGTCCCGCAACGAGCGCAACCTTGTCAATTAATGCCATC-ATTAGTTGGGCACTTTAA	1146	QY			
Db				Db			
QY	1134	TGAGACTCGCGTGACAAACCGGAGGAGGTGGGATGACGTCAGTCTCATGCGCCCTT	1193	QY			
Db				Db			
QY	1147	GGAGACTGCGAGTGAATACTGGAGAGGTGGGATGACGTCAGTCTCATGCGCCCTT	1206	QY			
Db				Db			
QY	1194	ATGGGTAGGGCTTACAGTGAATAAATGGGCGGTACAGAGGGTTGCCAACCGCGAGG	1253	QY			
Db				Db			
QY	1207	ACGAGTAGGGCTTACACAGTGTCTAATATGGGCGCATACAAAGAGAGCGACCTCGCGAG	1266	QY			
Db				Db			
QY	1254	GGAGCTAATCTCAGAAAGCGGCTGTGTCGAGATCGAGTCTGCAACTCGACTCCGTGA	1313	QY			
Db				Db			
QY	1267	CAAGCGGACCTCATAAAGTGGCTGTAGTCCGATTTGAGTCTGCACTCGACTCCATGA	1326	QY			
Db				Db			
QY	1314	AGTCGGAATCGCTAGTAAATCGCGGATCAGCATGTTCGCGGTGAATACGTTCCCGGTCTTG	1373	QY			
Db				Db			
QY	1327	AGTCGGAATCGCTAGTAAATCGTGGATCAGAAATGCCACCGTGAATACGTTCCCGGCTTG	1386	QY			
Db				Db			
QY	1374	TAACACCGCCGCTACACCATGGAGTGGGTTTACCAGAGAGAGATAGTCTAACCGT-	1432	QY			
Db				Db			
QY	1387	TACACCGCCGCTACACCATGGAGTGGGTTTGCAAAAGAGATAGTCTAACCTTC	1446	QY			
Db				Db			

RESULT 11
 US-10-831-286A-48678
 ; Sequence 48678, Application US/10831286A
 ; Publication No. US20060046246A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ZENG, QIANDONG
 ; APPLICANT: CHATELLIER, SONIA
 ; APPLICANT: MOIR, DONALD T.
 ; APPLICANT: LACROIX, BRUNA
 ; APPLICANT: CHILDRESS, DARRELL
 ; TITLE OF INVENTION: GENUS, GROUP, SPECIES AND/OR STRAIN SPECIFIC 16S rDNA SEQUENCES
 ; FILE REFERENCE: 032796-174.001
 ; CURRENT APPLICATION NUMBER: US/10/831,286A
 ; PRIOR FILING DATE: 2004-04-26
 ; PRIOR APPLICATION NUMBER: 60/464,955
 ; PRIOR FILING DATE: 2003-04-24
 ; NUMBER OF SEQ ID NOS: 48788
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 48678
 ; LENGTH: 1535
 ; TYPE: DNA
 ; ORGANISM: Proteus penneri
 US-10-831-286A-48678

Query Match 67.4%; Score 988.8; DB 9; Length 1535;
 Best Local Similarity 81.6%; Pred. No. 1.2e-294;
 Matches 1205; Conservative 0; Mismatches 262; Indels 9; Gaps 5;

QY	1	TTGATCATCGCTCAGATTGCAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACCGGAG	60	QY	61	CA----CGGGTGCTTGTGACCTTGTGCGAGTGGCGGAGTGGGTGAGTAATGATCGGAACG	116
Db				Db			
QY	6	TTGATCATCGCTCAGATTGCAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACCGGTA	65	QY	66	CAGAGAAAGCTTGTCTTCTGTCAGAGCGCGGACGGGTGAGTAATGATGCGGATC	125
Db				Db			
QY	117	TGTCAGAGAGTGGGGATAACGCATCGAAGATGTCTAATACCGCATATTTCTTACGGA	176	QY	126	TGCCCGATGAGGGGATAACTACTGGAACCGGTGGCTAATACCGCATGACGTCIACGGA	185
Db				Db			
QY	177	GGAAGCAGCGGATCGAAAGACCTTGTGCTTTTGGAGCGCCGATCCCTGATAGCTAGT	236	QY	186	CBAAGCAGGGGCTCTTCGGACCTTTCGGATGAACCCATATGGGATTAGCTAGT	245
Db				Db			
QY	237	TGTTGGGTTAAAGGCTTACCAAGGCAACGATCAGTAGTTGGTCTGAGAGACGACCGAC	296	QY	246	AGGTGAGGTAAGAGGCTCACCTAGCGACGATCTCTAGCTGGTCTGAGAGATGATCAGCC	305
Db				Db			
QY	297	ACACTGGGCTGAGACACCGCCAGACTCTACGGAGGCGAGCAGTGGGGAATTTTGGAC	356	QY	306	ACACTGGGCTGAGACACCGCCAGACTCTCTAAGGAGGCGAGCAGTGGGGAATTTGAC	365
Db				Db			
QY	357	AATGGCGAAGGCTTGATCCAGCAATCCGCGTGAAGTGAAGAGG-CTTCGGGTTGTAAA	415	QY	366	AATGGCGCAAGCCTTGATGCGCATCCGCGTGTATGAAGAGGCGCTTAGGGTTGTAAA	425
Db				Db			
QY	416	GCTCTTTTCACTCGAGAGAAAAGGTTGTGACTAATTAATCAAACTTATGATGTGACGAC	475	QY	426	GTACTTTTCACTCGAGAGAAAAGGTTGTGACTAATTAATCAAACTTATGATGTGACGAC	485
Db				Db			
QY	476	AGAAGAGCACCCTTAACCTACTGTCAGCAGCCGCGTAAATACGTAAGGTGCAAGCGTT	535	QY	486	AGAAGAGCACCCTTAACCTACTGTCAGCAGCCGCGTAAATACGTAAGGTGCAAGCGTT	545
Db				Db			
QY	536	AATCGGAATTAACCTGGGCGTAAAGGGTGCAGCGCGCTTTGTAAGTCAGATGTGAATATC	595	QY	546	AATCGGAATTAACCTGGGCGTAAAGGGTGCAGCGCGCTTTGTAAGTCAGATGTGAATATC	605
Db				Db			


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QY 596 CCGGCTTAACCTGGGAATTCGTTTGAACATAACAAAGCTAGAGTGTAGCAGAGGGGGT 655
Db 606 CCGAGCTTAACCTGGGAATTCGTTTGAACATAACAAAGCTAGAGTGTAGCAGAGGGGGT 665
QY 656 GGAATTCATGTAGCAGTGAATTCGTTAGAGATATGGAAGAAATCATGATGCGGAAGGC 715
Db 666 AGAATTCATGTAGCAGTGAATTCGTTAGAGATATGGAAGAAATCATGATGCGGAAGGC 725
QY 716 AGCCCTCTGGGTAAACCTGACGCTCATGCAAGAGGCTGGGAGCAACAGGATTAGA 775
Db 726 GGCCCTCTGGGAAAGACTGACGCTCAGTGGGAAGCGTGGGAGCAACAGGATTAGA 785
QY 776 TACCTGTGTAGTCCACGCCCTAAACGATGTC-AACTAGTGTGTGGGCCCTTACTAGCTTG 834
Db 786 TACCTGTGTAGTCCACGCCCTAAACGATGTCGATTTAGAGGTGTGGTCTTGAACCGTGG 845
QY 835 GTACGTAGCTAAACCGCTGAAGTTGACCGCTCTGGGGAGTACGCTCGCAGGATTTAAACCTC 894
Db 846 CTTCTGGAGCTAAACCGCTTAATTCGACCGCTCTGGGGAGTACGCTCGCAGGATTTAAACCTC 905
QY 895 AAAGGAATTTGACGGGGCCCGCACCAAGCGGTGGATTGTGATTAATTCGATGCAACGC 954
Db 906 AAATGAATTTGACGGGGCCCGCACCAAGCGGTGGAGCATGTGTTTAAATTCGATGCAACGC 965
QY 955 GAAAAACCTTACCTACCTTGACATGTAGCGAATAATTTAGAGATAAAATAGTGCCTTCG 1014
Db 966 GAAGAACCTTACCTTACTTCTGACATCCAGCGGATCTTTAGAGATAGAGGTGCTTCG 1025
QY 1015 GGAACGTAAACACAGGTGCTGATGCTGTGCTGACGTGCTGTGCTGTGAGATGTTGGGTTA 1074
Db 1026 GGAACGTGAGACAGGTGCTGATGCTGTGCTGACGTGCTGTGCTGTGAGATGTTGGGTTA 1085
QY 1075 AGTCCCGCAAGCGGCAACCTTGTCAATTAATGCGCA--TCATTTAGTTGGGCACTTTA 1132
Db 1086 AGTCCCGCAAGCGGCAACCTTGTCAATTAATGCGCA--TCATTTAGTTGGGCACTTTA 1145
QY 1133 ATGAGACTCGCGGTGACAAACCGGAGGAGGTGGGGATGAGCTCAAGTCTCATGGCCCT 1192
Db 1146 AGGAGACTCGCGGTGATTAACCGGAGGAGGTGGGGATGAGCTCAAGTCTCATGGCCCT 1205
QY 1193 TATGGGTAGGCTTCACACGTAAATAAATGCGCGGTACAGAGGGTTGCCAACCCCGGAGG 1252
Db 1206 TACGATAGGGCTACACACGTGCTACAAATGGCAGATACAAAGAGAGCGGACTCGGAGA 1265
QY 1253 GGGAGCTAATCTCAGAAAGCGGCTGTAGTCGGATCGGATCGGATCGGATCGGATCGGATCGG 1312
Db 1266 GCAAGCGGAATCTATAAAGTCTGTGATGCTGTGATGCTGTGATGCTGTGATGCTGTGATG 1325
QY 1313 AAGTCGGAATCGTAGTAATCGCGGATCAGCATGTGCGGGTGAATACGTTCCCGGGCTTT 1372
Db 1326 AAGTCGGAATCGTAGTAATCGTAGTAATCGTAGTAATCGTAGTAATCGTAGTAATCGTAGTA 1385
QY 1373 GTACACACCGCCGCTCACCATGAGGAGTGGTTTCCACGAGAGCAGATAGTCTAACCGT 1432
Db 1386 GTACACACCGCCGCTCACCATGAGGAGTGGTTTCCACGAGAGCAGATAGTCTAACCGT 1445
QY 1433 -AAGAGGGCGTTTGGCAGCGGAGATTCATGACTGG 1467
Db 1446 CGGAGGGCGCTTACCACCTTTGTGATTCATGACTGG 1481
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RESULT 12

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US-10-831-286A-48681
; Sequence 48681, Application US/10831286A
; Publication No. US20060046246A1
; GENERAL INFORMATION:
; APPLICANT: ZENG, QIANLONG
; APPLICANT: CHATELIER, SONIA
; APPLICANT: MOIR, DONALD T.
; APPLICANT: LACROIX, BRUNA
; APPLICANT: CHILDRESS, DARRELL
; TITLE OF INVENTION: GENUS, GROUP, SPECIES AND/OR STRAIN SPECIFIC 16S rDNA SEQUENCES
; FILE REFERENCE: 032796-174.001
```

```
; CURRENT APPLICATION NUMBER: US/10/831,286A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/464,955
; FILING DATE: 2003-04-24
; NUMBER OF SEQ ID NOS: 48788
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48681
; LENGTH: 1494
; TYPE: DNA
; ORGANISM: Pantoea dispersa
US-10-831-286A-48681
```

Query Match 67.1%; Score 984; DB 9; Length 1494;

Best Local Similarity 82.3%; Pred. No. 3.7e-293;

Matches 1202; Conservative 0; Mismatches 250; Indels 8; Gaps 6;

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QY 16 ATTGAACGCTGGCGGATGCTTTTACATGCAAGTCGAACGCGCAGCAGCG--GTGCTTGC 73
Db 1 ATTGAACGCTGGCGGATGCTTTTACATGCAAGTCGAACGCGCAGCAGCAGCAGAGAGCTTGC 60
QY 74 ACCT--GTTGGCGAGTGGCGGACGCGGTGAGTAATGCAATCGCAAGCTGTCCAGAACTGGG 131
Db 61 TCTTTGGGTGGCGAGTGGCGGACGCGGTGAGTAATGCTGTGGGAAACTGCCGATGAGGGG 120
QY 132 GATAACGCAATCGAAAGATGTCTAATACCGCATATTTCTACGAGAGGAAAGCAGCGGATC 191
Db 121 GATTAATCTGGAACCGGTAGCTAATACCGCATTAACGTCGCAGACCAAGATGGGGGACC 180
QY 192 GAAAGACCTTGTGCTTTTGGAGCGCGCATGCTGATTTAGCTAGTTGTGGGGTAAAGGC 251
Db 181 TTCGGGCTCACACCATCGATGTGCCAGATGGGATAGCTAGTAGTGGGGTAAATGCG 240
QY 252 CTACCAAGGCAACCATCATGATGTTGGTCTGAGAGAGCAACGACCACTGGGACTGAGA 311
Db 241 TCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGAGTACCAAGCAGCAGCTGGAACCTGAGA 300
QY 312 CACGGCCAGACTCCTCAGGAGGCGCAGCTGGGGAAATTTTGGCAATGGGCGAAAGCCT 371
Db 301 CACGGTCCAGACTCCTCAGGAGGCGCAGCTGGGGAAATTTTGGCAATGGGCGCAGGCT 360
QY 372 GATCCAGCAATGCGCGGTGAGTGAAGAGG--CTTCGGGTGTAAAGCTTTTCACTGCGAG 430
Db 361 GATGACGCAATGCGCGGTGATGAAGAGGCTTTCGGGTGTAAAGTACTTTTCACTGCGAG 420
QY 431 AAGAAAGGTTGTCACTAATTAATCACAACCTTATGATGTCGACAGAGAGCAGCAGCGC 490
Db 421 AGGAAGGCGGTGAGGTAAATTAACCTCGCGGATGACGTTACCCGAGAGAGCAGCAGCGC 480
QY 491 TAACTAGCTGCGCAGCAGCGCGTAAATACGTAGGTCGCAAGCGTTAAATCGGAATTTACTGG 550
Db 481 TAACTAGCTGCGCAGCAGCGCGTAAATACGTAGGTCGCAAGCGTTAAATCGGAATTTACTGG 540
QY 551 GCGTAAAGGTCGCGAGCGGCTTTGTAAGTCAGATGTGAATATCCCGGGCTTAACTGG 610
Db 541 GCGTAAAGGTCGCGAGCGGCTTCTTAAAGTCAGATGTGAATATCCCGGGCTTAACTGG 600
QY 611 GAATGCGTTTGAACCTACAAAGCTAGAGTGTAGCAGAGGGGGGTGGAAATTCATGCTGA 670
Db 601 GAATGCGTTTGAACCTAGAGGCTTGTAGTCTGTAGAGGGGGGTAGAAATTCAGAGTGA 660
QY 671 GCAGTGAATGCGTAGAGATATGAAGAAATCCGATGCGCAAGGCGAGCGCCCTGGGTTAA 730
Db 661 GCGGTGAATGCGTAGAGATCTGAGGAAATACCGGTGCGCAAGGGGGGGCTTGGACGNA 720
QY 731 CACTGACGCTCATGCAAGAAAGCGTGGGAGCAACAGGATTAGATACCTCGGTAGTCCA 790
Db 721 GACTGACGCTCAGGTGCGAAAGCGTGGGAGCAACAGGATTAGATACCTCGGTAGTCCA 780
QY 791 GCGCCTAAACGATGTCACTAGTTGTTGGGCTTACTAGGCTTGG--TAACTAGCTAAGC 849
Db 781 GCGCCTAAACGATGTCACTAGTTGTTGGGCTTACTAGGCTTGG--TAACTAGCTAAGC 840
QY 850 CGTGAAGTTGACCGCTCGGGGAGTACGCTCGCAGGATTTAAACTCAAGGAATTTGACGGG 909
```

Db	841	CGTTAAGTCGACCGCTGGGAGTACGGCGCAAGGTTAAAACTCAAATGAATTGACGG	900
Qy	910	GACCCGACAAAGCGGTGGATTATGTGATTAATTCGATGCAACGCGAAAAACCTTACCTA	969
Db	901	GGCCCGACAAAGCGGTGGAGCATGTGGTTTAAATTCGATGCAACGCGAAAAACCTTACCTG	960
Qy	970	CCCTTGACATGTAGCGAATATTTAGAGATAAATAATAGTGCCTTCGCGAAACGCTTAACACAG	1029
Db	961	GCCTTGACATCCAGAGAACTTAGCAGAGATGCTTTGGTGCCTTCGCGAACTCTGAGACAG	1020
Qy	1030	GTGCTGATGGCTGTGCTGACGTGCTGTCTGATGATGTTGGGTTAAGTCCGCAACGAGC	1089
Db	1021	GTGCTGATGGCTGTGCTGACGTGCTGTGTTGTTGAAATGTTGGGTTAAGTCCGCAACGAGC	1080
Qy	1090	GCAACCTTGCTATTAAATTCGCATC-ATTTAGTTGGGCACTTTAAATGAGACTGCCGGTGA	1148
Db	1081	GCAACCTTTATCTTTGTTGCCAGCGTTTCGGCGGGAACTCAAAGGAGACTGCCGGTGA	1140
Qy	1149	CAAAACGAGGAAAGGTGGGATGAGCTCAAGTCTCATGCGCCTTATGGGTAGGGCTTCA	1208
Db	1141	TAAACCGAGGAAAGGTGGGATGAGCTCAAGTCTCATGCGCCTTATGGGTAGGGCTTCA	1200
Qy	1209	CAGTAATACATGCGCGGTACAGAGGTTGCCAACCCGCGAGGGAGCTAATCTCAGA	1268
Db	1201	CAGTGTACAAATGGCGCATACAAAGAGAGCGACCTTCGCGAGAGCAAGCGGACCTATA	1260
Qy	1269	AAGCGGTGCTAGTCCGGATCGGAGTCTGCAACTCGAATCCGTTGAACTCGGAATCGCTAG	1328
Db	1261	AAGTGCCTGCTAGTCCGGATGGAGTCTGCAACTCGAATCCGTTGAACTCGGAATCGCTAG	1320
Qy	1329	TAAATCGCGGATACGATGTCGCGGTGAATACGTTTCCGCGGTCTTTGATACACACCGCGTC	1388
Db	1321	TAAATCGTAGATCAGAAATGCTACGCTGGAATACTGTTCCGCGGCTTTGATACACACCGCGTC	1380
Qy	1389	ACACCATGGGAGTGGGTTTACCAAGAGCAGATAGTCTAAACCGT-AAGAGGGCGTTTGCC	1447
Db	1381	ACACCATGGGAGTGGGTTTCAAAAGAAAGTAGTAGTCTTAACTTCGCGAGGGCGCTTACC	1440
Qy	1448	ACGCGGAGATTCATGACTGG	1467
Db	1441	ACTTTGTGATTCATGACTGG	1460
RESULT 13			
US-10-831-286A-48693			
; Sequence 48693, Application US/10831286A			
; Publication No. US20060046246A1			
; GENERAL INFORMATION:			
; APPLICANT: ZENG, QIANDONG			
; APPLICANT: CHATELLIER, SONIA			
; APPLICANT: MOIR, DONALD T.			
; APPLICANT: LACROIX, BRUNA			
; APPLICANT: CHILDRESS, DARRELL			
; TITLE OF INVENTION: GENUS, GROUP, SPECIES AND/OR STRAIN SPECIFIC 16S rDNA SEQUENCES			
; FILE REFERENCE: 032796-174.001			
; CURRENT APPLICATION NUMBER: US/10/831,286A			
; PRIOR FILING DATE: 2004-04-26			
; PRIOR APPLICATION NUMBER: 60/464,955			
; PRIOR FILING DATE: 2003-04-24			
; NUMBER OF SEQ ID NOS: 48788			
; SOFTWARE: PatentIn version 3.2			
; SEQ ID NO 48693			
; LENGTH: 1527			
; TYPE: DNA			
; ORGANISM: Morganella morganii sp. morganii			
US-10-831-286A-48693			
Query Match 67.1%; Score 983.8; DB 9; Length 1527;			
Best Local Similarity 81.9%; Ref. No. 4.3e-293;			
Matches 1208; Conservative 0; Mismatches 257; Indels 10; Gaps 6;			
Qy	3	GATCATGGCTCAGATTGAACGCTGGCGGCATGCTTTTA-CACATGCAAGTCGAACGGCAGC	61

Db	1	GATCATGGCTCAGATTGAACGCTGGCGGCAGCGCTTAAGCAATGCAAGTTCGGCGGTAAAC	60
Qy	62	ACGGGTGCTTGACAC---CTGGTGGCGAGTGGCGGACGGGTGAGTAATGATCGAATCGGAA	117
Db	61	AGGGAGAAAGCTTGTCTCTGCTGACGAGCGCGGACGGGTGAGTAATGATCGGCGATCT	120
Qy	118	GTCCAGAAAGTGGGGATTAACGATCGAAGATGTGCTAATACCGCATATCTCTACGGAG	177
Db	121	GCTGATGGCGGGGATTAACCTAGGAAACGGTAGCTAATACCGCATATGCTCTTCGGAC	180
Qy	178	GAAAGCAGGGGATCGAAAGACCTTGCTTTTGGAGCGCCGATGCTGATTAGCTAGT	237
Db	181	CAAGCGGGGAGCTTCGGGCTCGGCCATCAGATGAACCCATATGGGATTAGCTAGTA	240
Qy	238	GGTGGGTAAAGCCCTTACCAAGGCAACGATCAGTAGTGTGCTCTGAGAGGACGACGCA	297
Db	241	GCTGAGGTAAACGGCTTACCTAGGCGACGATCCCTAGCTGCTCTGAGAGGATGATCAGCA	300
Qy	298	CACTGGGACTGAGACACGCGCCAGACTCTCTACGGGAGGCGAGTGGGGAATTTTCGACA	357
Db	301	CACTGGGACTGAGACACGCGCCAGACTCTCTACGGGAGGCGAGTGGGGAATTTTCGACA	360
Qy	358	ATGGGCGAAAGCTCTGATCCAGCAATGCGCGCTGAGTGAAGAAAGG-CTTCGGGTGTAAAG	416
Db	361	ATGGGCGCAAGCTGATGCGCCATGCGCGGTGATGAAGAAAGGCTTCGGGTGTAAAG	420
Qy	417	CTCTTTCACTGAGAGAAAGAGGTGTGATCTAATATCAAACTTATGATGTTACCGACA	476
Db	421	TACTTTCACTGCGGAGAAAGGTGGCAAGGTAAATAACCTTGGCAATTTGACGTTACCGACA	480
Qy	477	GAGAGACACCGCTAACTACGTGCCAGCAGCGCGGTAAATACGTAGGGTGCAGCGTTA	536
Db	481	GAGAGACACCGCTAACTCTCGTCCAGCAGCGCGGTAAATACGTAGGGTGCAGCGTTA	540
Qy	537	ATCGGAATTAATCTGGCGTAAAGGTCGCGAGCGGCTTTGTAAGTCAGATGTGAATCCC	596
Db	541	ATCGGAATTAATCTGGCGTAAAGGTCGCGAGCGGCTTTGTAAGTCAGATGTGAATCCC	600
Qy	597	CGGGCTTAACCTGGGAATTCGGTTGAAACTCAAAAGCTAGAGTGTAGCAGAGGGGGTG	656
Db	601	CGGGCTTAACCCGGGAATTCGCATCTGATCTGCTAGCTAGAGTCTTTGAGAGGGGGTA	660
Qy	657	GAAATTCATGTGTAGCAGTGAATGCGTAGAGATATGGAAGAAACATCGATGGCGAAGGCA	716
Db	661	GAAATTCATGTGTAGCAGTGAATGCGTAGAGATATGGAAGAAACATCGATGGCGAAGGCG	720
Qy	717	GCCCCCTGGGTTAACTGACCGCTCATGCAAGCGTGGGGAGCAGCAACAGAGTTAGAT	776
Db	721	GCCCCCTGGCAAAAGACTGACCGCTCAGGTGCGAAAGCGTGGGGAGCAACAGAGTTAGAT	780
Qy	777	ACCTGTGTAGTCCACCGCTTAAACGATGTCAAC-TAGTTGTGGGCTTACTAGGCTTGG	835
Db	781	ACCTGTGTAGTCCACCGCTTAAACGATGTCACTTGGAGGTGTGCTTGGCGGCTGGC	840
Qy	836	TAACTGATGCTAAACGCGTGAAGTTGACCGCTGGGAGTACGGTGCAGAGTAATAAATCA	895
Db	841	TTCGGGAGCTAAACGCGTGAAGTCAACCGCTGGGAGTACGGCGCAAGGTGTAATACTCA	900
Qy	896	AAGGAATTAAGCGGGAGCCGACAAAGCGGTGGAATTAATGCGATTAAATTCGATCAACGCG	955
Db	901	AATGAATTAAGCGGGGGCCGCAACGCGGTGGAGCATGTGGTTTAAATTCGATCAACGCG	960
Qy	956	AAAAACCTTACCTTACCTTACATGATGCGAAATATTTAGAGATAAATAAGTGCCTTCGG	1015
Db	961	AAGAACCTTACCTTACCTTACATGATCCAGAACTTGGCAGAGATGCTTTGTCGCTTCGG	1020
Qy	1016	GAAACGCTTAACAGAGTGTGCTGATGGTGTGCTGATGCTGCTGATGATGTTGGGTAA	1075
Db	1021	GAACTCTGACACAGGTGCTGATGGTGTGCTGATGCTGCTGATGATGTTGGGTAA	1080
Qy	1076	GTCCCGCAACGAGCGCAACCTTGTCAATTAATTTGCCA--TCATTTAGTTGGGCACTTAA	1133

Db 1081 GTCCGCAACAGGCGCAACCTTATCTTTGTCAGCGGTGATGTCGGGAACTCAA 1140
Qy 1134 TGAGACTGCGGTGACAAACCGGAGGAGTGGGATGACGTCAAGTCTCATGSCCCTT 1193
Db 1141 GGAGACTGCGGTGATAAACCGGAGGAGTGGGATGACGTCAAGTCTCATGSCCCTT 1200
Qy 1194 ATGGGTAGGGCTTACACGTAATAACAATGGCGGTACAGAGGGTTGCCAACCCGCGAGGG 1253
Db 1201 ACGAGTAGGGCTACACACGTCTACAATGGCGGTATACAAAGGGAAGCGACCCGCGAGGG 1260
Qy 1254 GGAGCTAATCTCAGAAAGCGGTGCTAGTCCGGATCGAGTCTGCAACTCGACTCCGTGA 1313
Db 1261 CAAGCGGAACCTATAAAGTAGCTGCTAGTCCGGATGGAGTCTGCAACTCGACTCCATGA 1320
Qy 1314 AGTCGGAATCCCTAGTAATCCGGATCAGCATGTCGGGTGAATACGTTCCCGGGTCTTG 1373
Db 1321 AGTCGGAATCCCTAGTAATCCGGATCAGCATGTCGGGTGAATACGTTCCCGGGTCTTG 1380
Qy 1374 TACACACGCGCGTACACACCATGGAGTGGGTTTCCACAGAGCAGATAGTCTAACCC-GT 1432
Db 1381 TACACACGCGCGTACACACCATGGAGTGGGTTGCAAAAGAGTAGGTAGCTTAACCTCC 1440
Qy 1433 AAGAGGGGCTTTCACACGCGGAGATTCATGACTGG 1467
Db 1441 GGGAGGGCGCTTACCACCTTTGTGATTCATGACTGG 1475

RESULT 14

US-10-831-286A-48683
; Sequence 48683, Application US/10831286A
; Publication No. US20060046246A1
; GENERAL INFORMATION:
; APPLICANT: ZENG QIANDONG
; APPLICANT: CHATELLIER, SONIA
; APPLICANT: MOIR, DONALD T.
; APPLICANT: LACROIX, BRUNA
; APPLICANT: CHILDRESS, DARRELL
; TITLE OF INVENTION: GENUS, GROUP, SPECIES AND/OR STRAIN SPECIFIC 16S rDNA SEQUENCES
; FILE REFERENCE: 032796-174.001
; CURRENT APPLICATION NUMBER: US/10/831.286A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/464,955
; PRIOR FILING DATE: 2003-04-24
; NUMBER OF SEQ ID NOS: 48788
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48683
; LENGTH: 1493
; TYPE: DNA
; ORGANISM: Pantoea dispersa
US-10-831-286A-48683

Query Match 67.0%; Score 982.4; DB 9; Length 1493;

Best Local Similarity 82.3%; Pred. No. 1.2e-292;

Matches 1201; Conservative 0; Mismatches 251; Indels 8; Gaps 6;

Qy 16 ATTGAACGCTGGCGGCTTTTACACATGCAAGTCGAACCGCAGCAGCG--GTGCTTGC 73
Db 1 ATTGAACGCTGGCGGAGCCCTTACACATGCAAGTCGAACCGCAGCAGCTTGC 60
Qy 74 ACCT--GGTGGCGAGTGGCGGAGCGGTGAGTAATGTCATCGGAACGTTGCCAGAAAGTGGGG 131
Db 61 TCTTTGGTGGCGAGTGGCGGAGCGGTGAGTAATGTCGCGGAACCTGCCGATGGAGGGG 120
Qy 132 GATAACGATCGAAAGATGCTAATACCGGATATCTCTACGGAGGAAAGCAGGGGATC 191
Db 121 GATAACTACTGGAACCGGTAGCTAATACCGGATATACCGTAAACGTCGCAAGACCAAGTGGGGGACC 180
Qy 192 GAAAGACCTTGTCTTTTGGAGCGCGCATGCCCTGATTTAGCTAGTGTGGTGGGTAAAGGC 251
Db 181 TTCGGGCTTACACATCGGATGTGCCAGATGGATTTAGCTAGTGGGTAAATGGC 240
Qy 252 CTACCAAGGCAACGATCAGTATGTTGGTCTGAGAGGACGACCAAGCAGCAGCTGGGACTGAGA 311

Db 241 TCACCTAGGCGACGATCCCTAGCTGCTGAGAGGATGACCAGCCACACTGGAACCTGAGA 300
Qy 312 CACGSCCCAGACTCTCTACGGGAGCAGCAGTGGGGAATTTTGGCAATATGGGCGGAAGCCT 371
Db 301 CACGCTCAGACTCTCTACGGGAGCAGCAGTGGGGAATTTTGGCAATATGGGCGGAAGCCT 360
Qy 372 GATCCAGCAATGCCGCGTGAAGTGAAGAGG--CTTGGGTTGTAAAGCTCTTTTCACTCGAG 430
Db 361 GATGACGCCATGCCGCGGTATGAAGAGGCGCTTCGGGTTGTAAAGTACTTTTCACTCGAGG 420
Qy 431 AAGAAAAGGTTGCACTAATAATCACAATATATGATGTCGACAGAGAGAGACCGCCG 490
Db 421 AGAAGCGCGGTGAGTTAATAACCTTCCCGATTACGTTACCCGAGAGAGACCGCCG 480
Qy 491 TAACTGCTGTCACAGCGCGGTAAATACGTAGGTGCAAGCGTTAAATCGGAATTTACTTGG 550
Db 481 TAACTGCTGTCACAGCGCGGTAAATACGAGGGGTGCAAGCGTTAAATCGGAATTTACTTGG 540
Qy 551 GCGTAAAGGGTGGCAGCGCGCTTTTGAAGTCAGATGTGAATATCCCGGGCTTAACTCTGG 610
Db 541 GCGTAAAGCGCACCGCAGCGCGCTCTGTTAAGTCAGATGTGAATATCCCGGGCTTAACTCTGG 600
Qy 611 GAATTCGCTTTGAAACTACAAAGCTAGAGTGTAGAGGGGGGTGGAATTCATGTGTGA 670
Db 601 GAACTGCAATTTGAAACTGGCAGGCTTGAGTCTCGTAGAGGGGGGTAGAAATTCAGGTGTA 660
Qy 671 GCAGTGAATTCGCTAGAGATATGAAGAACATCGATGCGGAAGCAGCGCCCTCGGTGTTAA 730
Db 661 GCGGTGAATTCGCTAGAGATCTGGAGGAATACCGGTGCGGAAGCGCGCCCTCGTGAACGA 720
Qy 731 CACTGACGCTCATGCAAGAGCGTGGGGAGCAAAACAGGATTAGATACCTCTGTAGTCCA 790
Db 721 GACTGACGCTCAGTGCAGGAAGCGTGGGAGCAAAACAGGATTAGATACCTCTGTAGTCCA 780
Qy 791 GCGCTTAAACGATGTCAACTAGTTGTTGGGCTTACTAGGCTTGG--TAACTGATTAACG 849
Db 781 GCGCTTAAACGATGTCAACTGTTGGAGTGTGTCCTTGGAGCGTGGCTTCCGAGCTAACG 840
Qy 850 CGTGAAGTTGACCCCTGGGAGTACGCTGCGCAGGATTAAACCTCAAGGAATTCACCGG 909
Db 841 CGTTAAGTGCAGCCGCTGGGGAGTACGCGCCGCAAGGTTAAACCTCAAGTAATTTACCGG 900
Qy 910 GACCCGCAAGCGGTGGATTATGATGATTAATTCGATGCAACGCAAAAACCTTTACCTTA 969
Db 901 GCGCGCACAGCGGTGGAGCATGTGTTTAAATTCGATGCAACGCGAAGAACCTTTACCTG 960
Qy 970 CCCTTGACATGTACGGAATATTTTAGAGATAAATAGTGCCTTCGGGAAAGCGTAAACAG 1029
Db 961 GCCTTGACATCCAGAGAACTTAGCAGAGATGCTTTTGGTGCCTTCGGGAACTCTGAGACAG 1020
Qy 1030 GTGCTGATGGCTGCTGCTGCTGCTGAGATGTTGGGTTAAAGTCCCGCAACGAGC 1089
Db 1021 GTGCTGATGGCTGCTGCTGCTGCTGCTGAGTGTGGAATGTTGGGTAAAGTCCCGCAACGAGC 1080
Qy 1090 GCAACCTTGTCTAATAATGTCATC--ATTAGTTGGGCACCTTTAATGAGACTGCGCGTGA 1148
Db 1081 GCAACCTTATCTTGTGTCAGCGGTTGCGCGCGGNACTCAAGAGACTGCGCGTGA 1140
Qy 1149 CAACCGGAGGAAGGTGGGATGACGTCAAGTCTCATGCGCCCTTATGGGTAGGGCTTCA 1208
Db 1141 TAAACCGGAGGAAGGTGGGATGACGTCAAGTCTCATGCGCCCTTTCGCGCCAGGGCTACA 1200
Qy 1209 CACGTAATACAAATCGCGGTACAGAGGGTTGCCAACCCGCGAGGGGAGCTAATCTCAGA 1268
Db 1201 CACGTGTACAAATGGCGCATACAAAGAGAGAGCGACCTCGCGAGAGCAAGCGGACCTCAT 1260
Qy 1269 AAGCGCTGCTAGTTCGGATCGGAGTCTGCAACTCGACTCCGTTGAAGTCCGGAATCGCTAG 1328
Db 1261 AAGTGCCTGCTAGTCCGGATTGGAGTCTGCAACTCGACTCCATGAAGTCGGAATCGCTAG 1320
Qy 1329 TAATCGCGGATCAGCATGTGCGCGGTGAATAGCTTCCCGGGTCTTGTACACACCGCCCGTC 1388
Db 1321 TAATCGTAGATCAGAAATGCTACGCGTGAATAGCTTCCCGGGCTTGTACACACCGCCCGTC 1380

QY 1389 ACACATGGGAGTGGGTTTACACAGAGCAGATAGTCTAACCGT-AAGAGGGCGTTTGCC 1447
 Db 1381 ACACATGGGAGTGGGTTGCAAAAGAAAGTAGGTAGCTTAAACCTTCGGAGGGCGCTTACC 1440
 QY 1448 ACGCGGAGATTTCATGACTGG 1467
 Db 1441 ACTTTGTGATTCATGACTGG 1460

RESULT 15
 US-10-831-286A-48676
 ; Sequence 48676, Application US/10831286A
 ; Publication No. US20060046246A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ZENG, QIANDONG
 ; APPLICANT: CHATELLIER, SONIA
 ; APPLICANT: MOIR, DONALD T.
 ; APPLICANT: LACROIX, BRUNA
 ; APPLICANT: CHILDRESS, DARRELL
 ; TITLE OF INVENTION: GENUS, GROUP, SPECIES AND/OR STRAIN SPECIFIC 16S rDNA SEQUENCES
 ; FILE REFERENCE: 032796-174.001
 ; CURRENT APPLICATION NUMBER: US/10/831,286A
 ; PRIOR FILING DATE: 2004-04-26
 ; PRIOR APPLICATION NUMBER: 60/464,955
 ; PRIOR FILING DATE: 2003-04-24
 ; NUMBER OF SEQ ID NOS: 48788
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 48676
 ; LENGTH: 1494
 ; TYPE: DNA
 ; ORGANISM: Enterobacter hormaechei
 US-10-831-286A-48676

Query Match 66.7%; Score 979.2; DB 9; Length 1494;
 Best Local Similarity 82.1%; Pred. No. 1.1e-291;
 Matches 1199; Conservative 0; Mismatches 253; Indels 8; Gaps 6;

QY 16 ATTGAACGCTGGGGCGATGCTTTACACATGCAAGTCGAACGGCAGCAG--GGTGCTTGC 73
 Db 1 ATTGAACGCTGGGGCGAGGCTTAACACATGCAAGTCGAACGGTAAACAGGAGCAGCTTGC 60
 QY 74 ACCT--GGTGGCAGTGGCGGAGCGGTGAGTAAATGCAATCGGAACGTGTCCAGAAAGTGGGG 131
 Db 61 TGCTTGGCTGACAGTGGCGGAGCGGTGAGTAAATGCTGGAAGAACTGCTGATGGAGGG 120
 QY 132 GATAACGCATCGAAAGATGTGCTAATACCGCATATTCTTACGGAGGAAAGAGGGGATC 191
 Db 121 GATAACTACTGGAACCGGTAGCTAATACCGCATAAACGTGCAAGAGCCAAAGAGGGGAGCC 180
 QY 192 GAAAGACCTTGTGCTTTTGGAGCGCCGATGCTGATAGCTAGTTGGTGGGTTAAAGGC 251
 Db 181 TTCGGGCGCTTGTGCCATCGGATGTGCCAGATGGGATTTAGCTAGTAGTGGGTAAACGGC 240
 QY 252 CTACCAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACGACACCTGGGACTGAGA 311
 Db 241 TCACCTAGGCGACGATCCCTAGCTGCTGAGAGGATGACAGCCACACTGGAACTGAGA 300
 QY 312 CACGGCCACAGCTCTTACGGGAGGACGACGAGTGGGGAATTTTGGACAATGGCGGAAAGCCT 371
 Db 301 CACGGTCCAGACTCTTACGGGAGGACGACGAGTGGGGAATTTGACAAATGGCGCAAGCCT 360
 QY 372 GATCCAGCAATGCGCGTGTAGTAGAGG--CTTCGGGTTGTAAGCTCTTTTCAGTTCGAG 430
 Db 361 GATGCGACCATGCGCGGTGTATGAAGAAGGCTTTCGGGTTGTAAAGTACTTTTCAGCGGG 420
 QY 431 AAGAAAGGTTGTGACTAATAACCAACTTATGATGGTACCGACAGAAAGCACCGGC 490
 Db 421 AGAAGCGGATGAGTTTAATTAACCTCAGCAATTTGACGTTACCCGCAAGAAAGCACCGGC 480
 QY 491 TAACTACGTCGCCAGCAGCGCGGTAAATACGTAAGGTGCAAGCGTTAATCGGAATTAATCG 550
 Db 481 TAACTCGTCCAGCAGCGCGGTAAATACGTAAGGTGCAAGCGTTAATCGGAATTAATCG 540

QY 551 GCGTAAAGGGTGGCAGGCGGCTTTGTAAAGTCAGATGTGAAATCCCGGGCTTAAACCTGG 610
 Db 541 GCGTAAAGGCGCAGCAGGCGGCTGTGCAAGTCGATGTGAAATCCCGGGCTTAAACCTGG 600
 QY 611 GAATTGCGTTGAAACTACAAAGCTAGAGTGTAGCAGAGGGGGGTGGAATTCATATGTGTA 670
 Db 601 GAATCGATTTCGAAACTGGCAGGCTAGAGTCTTGTAGAGGGGGGTAGAAATCCAGGTGTA 660
 QY 671 GCAGTGAATTCGCTAGAGATATGGAAGAACATCGATGGCGAAGGAGCCGCCCTGGGTAA 730
 Db 661 GCGGTGAATTCGCTAGAGATCTGAGGAATACCGGTGGCGAAGGCGGCCCTGGACAAA 720
 QY 731 CACTGACGCTCATGCAAGAGCGTGGGAGCAAAACAGGATTTAGATACCTGCTAGTACCA 790
 Db 721 GACTGACGCTCAGGTGCGAAAGCGTGGGAGCAAAACAGGATTTAGATACCTGCTAGTACCA 780
 QY 791 CGCCCTAAACGATGTCAACTAGTGTGTGGGCTTACTAGGCTTGG--TAAAGTATAGCTAACG 849
 Db 781 CGCGGTAAACGATGTGACTTGGAGGTTGTGCCCTTGAGGCGTGGCTTCCGGAGCTAACG 840
 QY 850 CGTGAAGTTGACCGCCTGGGAGTACGGTGCAGGATTTAAACTCAAAGGAATTTGACGGG 909
 Db 841 CGTTAAGTCGACCGCCTGGGAGTACGGCGCAAGGTAAAACTCAAATGAATTTGACGGG 900
 QY 910 GACCCGCAAGCGGTGGATTTATGCGATTAAATTCGATGCAACGCGAAGAAACCTTACCTA 969
 Db 901 GCGCCGCAAGCGGTGGAGCTGTGGTTTAAATTCGATGCAACGCGAAGAAACCTTACCTA 960
 QY 970 CCCTTGACATGTAGCGAATATTTTAGAGATAAATAGTGCCTTCGCGGAAACGCTAACACAG 1029
 Db 961 CTCTTGACATCCAGAGAACTTAGCAGAGATGCTTGTGCTTCGCGAATCTCTGAGACAG 1020
 QY 1030 GTGCTGCATGGCTGTGCTGACGCTCGTGTGAGATGTTGGGTTAAAGTCCCGCAACGAGC 1089
 Db 1021 GTGCTGCATGGCTGTGCTGACGCTCGTGTGTTGTAATGTTGGGTTAAAGTCCCGCAACGAGC 1080
 QY 1090 GCACCCCTTGTCAATTAATGGCCATCATTTA--GTTGGGCACCTTTAAATGAGACTGCCGCTGA 1148
 Db 1081 GCACCCCTTATCTTGTGTTGCCAGCGGTTAGGCGGGAACTCAAAGGAGACTCCCACTGA 1140
 QY 1149 CAAACCGAGGAAGGTGGGAGTGAACGTCGCTCATGCGCCCTTATGGGTAGGGCTTCA 1208
 Db 1141 TAAACTGGAGGAAGGTGGGATGACGTCGCTCAAGTCATCATGCGCCCTTACGAGTAGGGCTACA 1200
 QY 1209 CAGCTAATTAATGGCGCGTACAGAGGTTGCCAACCCGGGAGGGGAGCTAATCTCAGA 1268
 Db 1201 CAGCTGCTACAATGGCGCATACAAAGAGAAGCGACCTCGCGAGAGCAAGCGGACCTCAT 1260
 QY 1269 AAGCGCTGTAGTCCGGATCGAGTCTGCAACTCGACTCCGTAAGTCCGGAATCGCTAG 1328
 Db 1261 AAGTGGCTGTAGTCCGGATTTGAGTCTGCACTGCTCACTCCATGAAAGTCCGGAATCGCTAG 1320
 QY 1329 TAATCCGGATCAGCATGTGCGGGTGAATACGTTCCCGGGTCTTTGTACACACCGCCGCTC 1388
 Db 1321 TAATCGTGGATCAGAATGCCAGGTGAATACGTTCCCGGGCTTTGTACACACCGCCGCTC 1380
 QY 1389 ACACATGGGAGTGGGTTTCAACGAGAGCAGATAGTCTAACCGT--AAGAGGGGCTTTGCC 1447
 Db 1381 ACACATGGGAGTGGGTTTCAAAAGAAAGTAGGTAGCTTAAACCTTCGGGAGGGCGCTTACC 1440
 QY 1448 ACGGCGAGATTTCATGACTCG 1467
 Db 1441 ACTTTGTGATTCATGACTCG 1460

Search completed: April 6, 2006, 21:15:08
 Job time : 772 secs

Db 181 AGCAGGGGATCGAAGACCTTGTGCTTTTGGAGCGGCGATGCTGCTGATTAGCTAGTTGGT 240
Qy 241 GGGGTAAGGCTTACCAAGCAACGATCAGTAGTTGGTCTGAGAGGACGACACGACAC 300
Db 241 GGGGTAAGGCTTACCAAGCAACGATCAGTAGTTGGTCTGAGAGGACGACACGACAC 300
Qy 301 TGGGACTGAGACAGCGGCCAGCTCTACGGGAGGAGCAGTGGGAAATTTTGGACAATG 360
Db 301 TGGGACTGAGACAGCGGCCAGCTCTCTACGGGAGGAGCAGTGGGAAATTTTGGACAATG 360
Qy 361 GGGCAAGCCTGATCCAGCAATCCGCGTGAGTGAAGAGGCTTCGGGTGTAAGCTCT 420
Db 361 GGGCAAGCCTGATCCAGCAATCCGCGTGAGTGAAGAGGCTTCGGGTGTAAGCTCT 420
Qy 421 TTCACTCGAGAGAAAGGTTGTGACTAATAATCAACAATTATGATGCTACCGACAGAAG 480
Db 421 TTCACTCGAGAGAAAGGTTGTGACTAATAATCAACAATTATGATGCTACCGACAGAAG 480
Qy 481 AAGCACCGCTTAACCTAGCTGCGACGCGCGGTAAATACGTAGGGTCAAGCGTTAATCG 540
Db 481 AAGCACCGCTTAACCTAGCTGCGACGCGCGGTAAATACGTAGGGTCAAGCGTTAATCG 540
Qy 541 GAATTAATCGGCGTAAAGGTTGCGAGCGGCTTTTGAAGTCAAGTGTGAATCCCGGG 600
Db 541 GAATTAATCGGCGTAAAGGTTGCGAGCGGCTTTTGAAGTCAAGTGTGAATCCCGGG 600
Qy 601 CTTAACCTGGAAATGCGTTTGAACCTACAAAGCTAGAGTGTAGCAGAGGGGTGGAAT 660
Db 601 CTTAACCTGGAAATGCGTTTGAACCTACAAAGCTAGAGTGTAGCAGAGGGGTGGAAT 660
Qy 661 TCCATGTGTAGCAGTGAATCGTAGAGATATGGAAGAAATCGATGGCGAAGCGACCCC 720
Db 661 TCCATGTGTAGCAGTGAATCGTAGAGATATGGAAGAAATCGATGGCGAAGCGACCCC 720
Qy 721 CTTGGGTTAACTGACCTATGCAAGAGCTGCGGAGCGCAACAGGATTTAGATACCC 780
Db 721 CTTGGGTTAACTGACCTATGCAAGAGCTGCGGAGCGCAACAGGATTTAGATACCC 780
Qy 781 TGGTAGTCCAGCCCTAAACGATGTCAACTAGTTGTTGGGCTTTACTAGGCTTGGTAACG 840
Db 781 TGGTAGTCCAGCCCTAAACGATGTCAACTAGTTGTTGGGCTTTACTAGGCTTGGTAACG 840
Qy 841 TAGCTAAACGCTGAGTTGACCGCTGGGGAGTAGCGTTCGAGGATTAATACTCAAAGGA 900
Db 841 TAGCTAAACGCTGAGTTGACCGCTGGGGAGTAGCGTTCGAGGATTAATACTCAAAGGA 900
Qy 901 ATTGACGGGACCCGCAACAGCGGTGGATATGTGGATTAAATTCGATGCAACGCGAATA 960
Db 901 ATTGACGGGACCCGCAACAGCGGTGGATATGTGGATTAAATTCGATGCAACGCGAATA 960
Qy 961 CCTTACCTACCTGACATGAGCAATATTTTAGAGATAAATAGTCCCTTCGGGACG 1020
Db 961 CCTTACCTACCTGACATGAGCAATATTTTAGAGATAAATAGTCCCTTCGGGACG 1020
Qy 1021 CTAACACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
Db 1021 CTAACACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
Qy 1081 GCACGAGCGCAACCTTGTCAATTAATTCCTATCAATTTAGTTGGGACCTTTAATGAGACT 1140
Db 1081 GCACGAGCGCAACCTTGTCAATTAATTCCTATCAATTTAGTTGGGACCTTTAATGAGACT 1140
Qy 1141 GCGGTTGACAAACCGGAGAGGTTGGGATGAGCTCAAGTCTCATGCGCTTATGGGTA 1200
Db 1141 GCGGTTGACAAACCGGAGAGGTTGGGATGAGCTCAAGTCTCATGCGCTTATGGGTA 1200
Qy 1201 GGGCTTCAACGTAATCAATGCGCGTACAGAGGGTTGCCAACCCGCGAGGGGAGCTA 1260
Db 1201 GGGCTTCAACGTAATCAATGCGCGTACAGAGGGTTGCCAACCCGCGAGGGGAGCTA 1260
Qy 1261 ATCTCAGAAAGCGCGTGTAGTCCGAGTCCGAGTCTGCACTCCGCTCGTAAGTCCGA 1320
Db 1261 ATCTCAGAAAGCGCGTGTAGTCCGAGTCCGAGTCTGCACTCCGCTCGTAAGTCCGA 1320

Qy 1321 ATCCCTAGTAAATCCGCGATCAGCATGTCGGGTGAATACGTTCCCGGGTCTTGTACACAC 1380
Db 1321 ATCCCTAGTAAATCCGCGATCAGCATGTCGGGTGAATACGTTCCCGGGTCTTGTACACAC 1380
Qy 1381 GCGCGTCAACCAATGGGAGTGGGTTTCCACAGAGCAGATAGTCTAACCCGTAAGAGGCG 1440
Db 1381 GCGCGTCAACCAATGGGAGTGGGTTTCCACAGAGCAGATAGTCTAACCCGTAAGAGGCG 1440
Qy 1441 GTTGGCCACCGCGAGATTTCATGACTGG 1467
Db 1441 GTTGGCCACCGCGAGATTTCATGACTGG 1467

RESULT 2
US-10-659-980A-18
; Sequence 18, Application US/10659980A
; Publication No. US20040106133A1
; GENERAL INFORMATION:
; APPLICANT: Hovanec, Timothy A
; TITLE OF INVENTION: Method for Detecting Ammonia-Oxidizing Bacteria
; FILE REFERENCE: 81289-284781
; CURRENT APPLICATION NUMBER: US/10/659,980A
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: US 09/573,684
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 60/386,217
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,218
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,219
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 1467
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: N. Aestuarii-like AOB P4c1one42 16S rDNA
US-10-659-980A-18

Query Match 100.0%; Score 1467; DB 7; Length 1467;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1467; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGATCATGCTCAGATTGCAAGCTGGCGGCATGCTTTTACATATGCAAGTCGAAACGGCAG 60
Db 1 TTGATCATGCTCAGATTGCAAGCTGGCGGCATGCTTTTACATATGCAAGTCGAAACGGCAG 60
Qy 61 CACGGGTGCTTGCACCTGTGGCGAGTGGCGGAGTGAATGATCGATCGGAACGTGTC 120
Db 61 CACGGGTGCTTGCACCTGTGGCGAGTGGCGGAGTGAATGATCGATCGGAACGTGTC 120
Qy 121 CAGAACTGGGGGATAACGATCGAAAGATGTCTAATACCGCATATTTCTACGGAGGAA 180
Db 121 CAGAACTGGGGGATAACGATCGAAAGATGTCTAATACCGCATATTTCTACGGAGGAA 180
Qy 181 AGCAGGGGATCGAAAGACCTTTGTGCTTTTGGAGCGGCGATGCTGATTTAGCTAGTTGGT 240
Db 181 AGCAGGGGATCGAAAGACCTTTGTGCTTTTGGAGCGGCGATGCTGATTTAGCTAGTTGGT 240
Qy 241 GGGGTAAGGCTTACCAAGCAACGATCAGTAGTTGGTCTGAGAGGACGACCGACACAC 300
Db 241 GGGGTAAGGCTTACCAAGCAACGATCAGTAGTTGGTCTGAGAGGACGACCGACACAC 300
Qy 301 TGGGACTGAGACAGCGGCCAGACTCTCTACCGGGAGGACGAGTGGGAAATTTTGGACAATG 360
Db 301 TGGGACTGAGACAGCGGCCAGACTCTCTACCGGGAGGACGAGTGGGAAATTTTGGACAATG 360
Qy 361 GCGGAAAGCCTGATCCAGCAATCCGCGTGTGAGTGAAGAGGCTTCGGGTGTAAGCTCT 420
Db 361 GCGGAAAGCCTGATCCAGCAATCCGCGTGTGAGTGAAGAGGCTTCGGGTGTAAGCTCT 420

Qy 421 TTCAAGTCGAGAGAAAGGTTGTGACTAATAATCAAACTTATGATGGTACCGACAGAG 480
 Db 421 TTCAAGTCGAGAGAAAGGTTGTGACTAATAATCAAACTTATGATGGTACCGACAGAG 480
 Qy 481 AAGCACCAGGCTAACTAGTCGACAGAGCCGCGTAATACGTAGGGTGCAACGGTTAATCG 540
 Db 481 AAGCACCAGGCTAACTAGTCGACAGAGCCGCGTAATACGTAGGGTGCAACGGTTAATCG 540
 Qy 541 GAATTAAGTCGAGAGAAAGGTTGTGACTAATAATCAAACTTATGATGGTACCGACAGAG 600
 Db 541 GAATTAAGTCGAGAGAAAGGTTGTGACTAATAATCAAACTTATGATGGTACCGACAGAG 600
 Qy 601 CTTAACTCTGGGAAATGCGTTTGAACATCAAAAGCTAGAGTGTAGCAGAGGGGGTGAAT 660
 Db 601 CTTAACTCTGGGAAATGCGTTTGAACATCAAAAGCTAGAGTGTAGCAGAGGGGGTGAAT 660
 Qy 661 TCCATGTGTAGCAGTAAATCGGTAGAGATATGAAGAACATCGATGGCGAAGGCAGGCC 720
 Db 661 TCCATGTGTAGCAGTAAATCGGTAGAGATATGAAGAACATCGATGGCGAAGGCAGGCC 720
 Qy 721 CCTGGGTAAACACTGACGCTCATGCAAGAGCGTGGGAGCAACAGGATTAGATACCC 780
 Db 721 CCTGGGTAAACACTGACGCTCATGCAAGAGCGTGGGAGCAACAGGATTAGATACCC 780
 Qy 781 TGGTAGTCCAGCCCTAAACGATGTCAACTAGTTGTTGGGCTTACTAGGCTTGGTAAACG 840
 Db 781 TGGTAGTCCAGCCCTAAACGATGTCAACTAGTTGTTGGGCTTACTAGGCTTGGTAAACG 840
 Qy 841 TAGCTAAACGCGTGAAGTGAACCGCTCGGGAGTAGCGTTCGAGGATTAAACCTCAAGGA 900
 Db 841 TAGCTAAACGCGTGAAGTGAACCGCTCGGGAGTAGCGTTCGAGGATTAAACCTCAAGGA 900
 Qy 901 ATTGACCGGAGCCGCAACAGCGGTGATATGTTGGATTAATTCGATGCAACCGCAAAA 960
 Db 901 ATTGACCGGAGCCGCAACAGCGGTGATATGTTGGATTAATTCGATGCAACCGCAAAA 960
 Qy 961 CTTTACCTACCTTGAATGATGAGGATATTTAGAGATAAATAGTGCCTTCGGGAAACG 1020
 Db 961 CTTTACCTACCTTGAATGATGAGGATATTTAGAGATAAATAGTGCCTTCGGGAAACG 1020
 Qy 1021 CTAAACAGGTCGATGAGGTCGTCAGCTCGTGTGAGATGTTGGGTTAAGTCCC 1080
 Db 1021 CTAAACAGGTCGATGAGGTCGTCAGCTCGTGTGAGATGTTGGGTTAAGTCCC 1080
 Qy 1081 GCAACGAGCGCAACCTTGTCAATTAATGCGATCAATTTAGTGGGCACTTTAATGAGACT 1140
 Db 1081 GCAACGAGCGCAACCTTGTCAATTAATGCGATCAATTTAGTGGGCACTTTAATGAGACT 1140
 Qy 1141 GCCGGTGACAAAACCGAGGAGGTTGGGATGACGTCAGTCAAGTCTCATGSCCTTATGGGTA 1200
 Db 1141 GCCGGTGACAAAACCGAGGAGGTTGGGATGACGTCAGTCAAGTCTCATGSCCTTATGGGTA 1200
 Qy 1201 GGGCTTCAACAGTAATAAATGCGCGCTACAGAGGGTTGCCAACCCGCGAGGGGAGCTA 1260
 Db 1201 GGGCTTCAACAGTAATAAATGCGCGCTACAGAGGGTTGCCAACCCGCGAGGGGAGCTA 1260
 Qy 1261 ATCTCAGAAAGCGGTCGTAGTCGGATCGGAGTCTGGAATCGACTCCGTTGAAGTCGGA 1320
 Db 1261 ATCTCAGAAAGCGGTCGTAGTCGGATCGGAGTCTGGAATCGACTCCGTTGAAGTCGGA 1320
 Qy 1321 ATCGCTAGTAATCGCGGATCAGCATGTCGGGTCAATACGTTCCGGGTCTTGTACACAC 1380
 Db 1321 ATCGCTAGTAATCGCGGATCAGCATGTCGGGTCAATACGTTCCGGGTCTTGTACACAC 1380
 Qy 1381 CGCCCGTCACACCAATGGGAGTGGGTTTCCACAGAGCAGATAGTCTAACCGTTAAGAGGGC 1440
 Db 1381 CGCCCGTCACACCAATGGGAGTGGGTTTCCACAGAGCAGATAGTCTAACCGTTAAGAGGGC 1440
 Qy 1441 GTTTGCCACGCGGAGATTCAATGACTGG 1467
 Db 1441 GTTTGCCACGCGGAGATTCAATGACTGG 1467

RESULT 3
 US-10-659-983A-18
 ; Sequence 18, Application US/10659983A
 ; Publication No. US2004015713A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hovanec, Timothy A
 ; TITLE OF INVENTION: Ammonia-Oxidizing Bacteria
 ; FILE REFERENCE: 81289-284779
 ; CURRENT APPLICATION NUMBER: US/10/659,983A
 ; CURRENT FILING DATE: 2003-09-10
 ; PRIOR APPLICATION NUMBER: US 09/573,684
 ; PRIOR FILING DATE: 2000-05-19
 ; PRIOR APPLICATION NUMBER: US 60/386,217
 ; PRIOR FILING DATE: 2002-09-19
 ; PRIOR APPLICATION NUMBER: US 60/386,218
 ; PRIOR FILING DATE: 2002-09-19
 ; PRIOR APPLICATION NUMBER: US 60/386,219
 ; PRIOR FILING DATE: 2002-09-19
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 18
 ; LENGTH: 1467
 ; TYPE: DNA
 ; ORGANISM: Unknown
 ; FEATURE:
 ; OTHER INFORMATION: N. aestuarii-like AOB P4clone42 16S rDNA
 US-10-659-983A-18

Query Match 100.0%; Score 1467; DB 7; Length 1467;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1467; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TTGATCATGCTCAGATTGAACGCTGGCGGATGCTTTACATGCAAGTGCACGGCAG 60
 Db 1 TTGATCATGCTCAGATTGAACGCTGGCGGATGCTTTACATGCAAGTGCACGGCAG 60
 Qy 61 CACGGGTGCTTGACCTGGTGGGAGTGGCGAGCGGTGAGTAAATGCAATCGGAACGTGC 120
 Db 61 CACGGGTGCTTGACCTGGTGGGAGTGGCGAGCGGTGAGTAAATGCAATCGGAACGTGC 120
 Qy 121 CAGAAGTGGGGGATTAACGCAATCGAAAGATGTGCTAAATACCGCATATTTCTTACGAGGAA 180
 Db 121 CAGAAGTGGGGGATTAACGCAATCGAAAGATGTGCTAAATACCGCATATTTCTTACGAGGAA 180
 Qy 181 AGCAGGGGATCGAAAGACCTTGTGCTTTTGGAGCGCGCGATGCCCTGATTAGTGGT 240
 Db 181 AGCAGGGGATCGAAAGACCTTGTGCTTTTGGAGCGCGCGATGCCCTGATTAGTGGT 240
 Qy 241 GGGTAAAGCCCTTACCAAGGCAACGATCAGTGTGCTGTGAGAGGACGACCGACACAC 300
 Db 241 GGGTAAAGCCCTTACCAAGGCAACGATCAGTGTGCTGTGAGAGGACGACCGACACAC 300
 Qy 301 TGGGACTGAGACACGCGCCAGACTCTTACGCGGAGGCGAGCAGTGGGGAAATTTTGGACAATG 360
 Db 301 TGGGACTGAGACACGCGCCAGACTCTTACGCGGAGGCGAGCAGTGGGGAAATTTTGGACAATG 360
 Qy 361 GCGAAAGCCCTGATCCAGCAATGCCGCTGAGTGAAGAAGGCTTCGGGTTGTAAGCTCT 420
 Db 361 GCGAAAGCCCTGATCCAGCAATGCCGCTGAGTGAAGAAGGCTTCGGGTTGTAAGCTCT 420
 Qy 421 TTCACTCGAGAAGAAAAGTTGTGACTAATAATCACAACCTTATGATGGTACCGACAGAG 480
 Db 421 TTCACTCGAGAAGAAAAGTTGTGACTAATAATCACAACCTTATGATGGTACCGACAGAG 480
 Qy 481 AAGCACCAGGCTAACTAGTCCAGCAGCCCGGTAATACGTAGGGTGCACGGCTTAATCG 540
 Db 481 AAGCACCAGGCTAACTAGTCCAGCAGCCCGGTAATACGTAGGGTGCACGGCTTAATCG 540
 Qy 541 GAATTAAGTCGAGAGAAAGGTTGGTAAAGTGGCGAGCGGCTTTGTAAGTCAGATGTAATCCCGGG 600
 Db 541 GAATTAAGTCGAGAGAAAGGTTGGTAAAGTGGCGAGCGGCTTTGTAAGTCAGATGTAATCCCGGG 600

Db 963 ACCTTACCTACCTTGACATGTAGCAATATTTTAGAGATAAAATAGTGCCTTCGGGAAC 1022
Qy 1020 GCTAAACACAGGTGCTGATGGCTGTGCTGAGCTGCTGCTGATGATGTTGGTTAAGTCC 1079
Db 1023 GCTAAACACAGGTGCTGATGGCTGTGCTGAGCTGCTGCTGATGATGTTGGTTAAGTCC 1082
Qy 1080 CGCAACGAGCGCAACCTTGTCAATTAATGCCATCATTTAGTTGGGCACCTTTAATGAGAC 1139
Db 1083 CGCAACGAGCGCAACCTTGTCAATTAATGCCATCATTTAGTTGGGCACCTTTAATGAGAC 1142
Qy 1140 TGGCGGTGACAAAACCGAGGAAGGTGGGATGACGTCAGTCTCATGCGCCCTTATGGGT 1199
Db 1143 TGGCGGTGACAAAACCGAGGAAGGTGGGATGACGTCAGTCTCATGCGCCCTTATGGGT 1202
Qy 1200 AGGCTTCACACGTAATACAAATGGCGGTACAGAGGTTGCCAAACCGCGAGGGGAGCT 1259
Db 1203 AGGCTTCACACGTAATACAAATGGCGGTACAGAGGTTGCCAAACCGCGAGGGGAGCT 1262
Qy 1260 AATCTCAGAAAGCGCTCGTAGTCCGATCCGATCGAGTCTGCAACTCGACTCCGCGAAGTCGG 1319
Db 1263 AATCTCAGAAAGCGCTCGTAGTCCGATCCGATCGAGTCTGCAACTCGACTCCGCGAAGTCGG 1322
Qy 1320 AATCGCTAGTAATCGCGGATCAGCATGTCGGGTGAATAGCTTCCCGGCTTGTACACA 1379
Db 1323 AATCGCTAGTAATCGCGGATCAGCATGTCGGGTGAATAGCTTCCCGGCTTGTACACA 1382
Qy 1380 CCGCCCGTCACACCATGGAGTGGTTCACCAAGACAGATAGCTTAACCGGTAA-GAGG 1438
Db 1383 CCGCCCGTCACACCATGGAGTGGTTCACCAAGACAGATAGCTTAACCGGTAAAGGAGG 1442
Qy 1439 GCGTTTGCCACGCGGAGATTCATGACTGG 1467
Db 1443 GCGTTTGCCACGCTGAGATTATGACTGG 1471

RESULT 6

US-10-659-983A-20
; Sequence 20, Application US/10659983A
; Publication No. US20040157313A1
; GENERAL INFORMATION:
; APPLICANT: Hovavac, Timothy A
; TITLE OF INVENTION: Ammonia-Oxidizing Bacteria
; FILE REFERENCE: 81289-284779
; CURRENT APPLICATION NUMBER: US/10/659,983A
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: US 09/573,684
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 60/386,217
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,218
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,219
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 1491
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: N. Aestuarii-like AOB BF16clone57 16S rDNA
US-10-659-983A-20

Query Match 98.2%; Score 1440.2; DB 7; Length 1491;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1464; Conservative 0; Mismatches 3; Indels 2; Gaps 2;
Qy 1 TTGATCATGGCTCAGATTGAACGCTGGCGCATGCTTTACACATGCAAGTCCGAACGGCAG 60
Db 3 TTGATCATGGCTCAGATTGAACGCTGGCGCATGCTTTACACATGCAAGTCCGAACGGCAG 62
Qy 61 CACGGGTGCTTCCACCTGCTGGCGAGTGGCGGACGCGGTGAGTAATCGGAACGCTGTC 120

Db 63 CACGGGTGCTTGCACCTGGTGGCGAGTGGCGGACGGGTGAGTAATGATCGGAACGTGTC 122
Qy 121 CAGAAGTGGGGGATAAACGATCGAAGATGTCTAATAACGATATTTCTTACGGAGGAA 180
Db 123 CAGAAGTGGGGGATAAACGATCGAAGATGTCTAATAACGATATTTCTTACGGAGGAA 182
Qy 181 AGCAGGGGATCGAAAGACCTTGTGCTTTGGAGCGCGGATGCTGATTTAGTAGTGGT 240
Db 183 AGCAGGGGATCGAAAGACCTTGTGCTTTGGAGCGCGGATGCTGATTTAGTAGTGGT 242
Qy 241 GGGGTAAAGGCTTACCAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACGAGCCACAC 300
Db 243 GGGGTAAAGGCTTACCAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACGAGCCACAC 302
Qy 301 TGGGATCGAGACACGGCCGACGACTCTTACGGGAGCAGCAGTGGGGAATTTTGGCAATG 360
Db 303 TGGGATCGAGACACGGCCGACGACTCTTACGGGAGCAGCAGTGGGGAATTTTGGCAATG 362
Qy 361 GGGGAAGCCCTGATCCAGCAATGCCGCTGAGTGAAGAAGG-CTTCGGGTGTGTAAGCTC 419
Db 363 GGGGAAGCCCTGATCCAGCAATGCCGCTGAGTGAAGAAGGCTTCGGGTGTGTAAGCTC 422
Qy 420 TTTCAAGTCGAGAAAGAAAGGTTGTGCACTAATAATCAAACTTATGATGGTACCGACAGAA 479
Db 423 TTTCAAGTCGAGAAAGAAAGGTTGTGCACTAATAATCAAACTTATGATGGTACCGACAGAA 482
Qy 480 GAAGCACCGGCTTAACCTACGTCGACGACGCGGCTAATACGTAGGTGCAAGCGTTAATC 539
Db 483 GAAGCACCGGCTTAACCTACGTCGACGACGCGGCTAATACGTAGGTGCAAGCGTTAATC 542
Qy 540 GGAATTTACTTGGCGGTAAAGGGTGGCGAGCGGCTTTGTAAAGTCAGATGTGAAATCCCCGG 599
Db 543 GGAATTTACTTGGCGGTAAAGGGTGGCGAGCGGCTTTGTAAAGTCAGATGTGAAATCCCCGG 602
Qy 600 GCTTAACTCTGGGAAATTCGCTTTGAAAACCTACAAAGCTAGAGTACGAGAGGGGGTGGAA 659
Db 603 GCTTAACTCTGGGAAATTCGCTTTGAAAACCTACAAAGCTAGAGTACGAGAGGGGGTGGAA 662
Qy 660 TTTCCATGTGTAGCAGTGAATTCGTAGAGATATGGAAGAACATCGATGGCGAAGGCGAGCC 719
Db 663 TTTCCATGTGTAGCAGTGAATTCGTAGAGATATGGAAGAACATCGATGGCGAAGGCGAGCC 722
Qy 720 CCTGGGTTTAACTGACGCTCATGCAACAAAGCTGGGGAGCAACACAGATTAGATACC 779
Db 723 CCTGGGTTTAACTGACGCTCATGCAACAAAGCTGGGGAGCAACACAGATTAGATACC 782
Qy 780 CTGGTAGTCCAGCCCTTAAACGATGTCAACTAGTTGCTTGGGCTTACTAGGCTTGGTAAC 839
Db 783 CTGGTAGTCCAGCCCTTAAACGATGTCAACTAGTTGCTTGGGCTTACTAGGCTTGGTAAC 842
Qy 840 GTAGCTAAACGCGTGAAGTTGACCGCTGGGGAGTACGGTGGCAGGATTTAAACTCAAAGG 899
Db 843 GTAGCTAAACGCGTGAAGTTGACCGCTGGGGAGTACGGTGGCAGGATTTAAACTCAAAGG 902
Qy 900 AATTGACGGGGACCCGACACAGCGGTGATATGTGGATTAATTCGATGCAACCGCAAAA 959
Db 903 AATTGACGGGGACCCGACACAGCGGTGATATGTGGATTAATTCGATGCAACCGCAAAA 962
Qy 960 ACCTTACCTACCTTGCACATGTAGCGAATATTTTAGAGATAAAATAGTGCCTTCGGGAAC 1019
Db 963 ACCTTACCTACCTTGCACATGTAGCGAATATTTTAGAGATAAAATAGTGCCTTCGGGAAC 1022
Qy 1020 GCTAAACACAGGTGCTGATGGCTGTGCTGAGTCTGCTGAGATGTTGGGTAAAGTCC 1079
Db 1023 GCTAAACACAGGTGCTGATGGCTGTGCTGAGTCTGCTGAGATGTTGGGTAAAGTCC 1082
Qy 1080 CGMAACGAGCGCAACCTTGTCAATTAATGCCATCATTTAGTTGGGACATTTAATGAGAC 1139
Db 1083 CGMAACGAGCGCAACCTTGTCAATTAATGCCATCATTTAGTTGGGACATTTAATGAGAC 1142
Qy 1140 TGGCGGTGACAAAACCGGAGGAAGGTGGGATGACGTCAGTCTCATAGTCTCTATGGCCCTTATGGGT 1199
Db 1143 TGGCGGTGACAAAACCGGAGGAAGGTGGGATGACGTCAGTCTCTATGGCCCTTATGGGT 1202

QY 1380 CCGCCGTCACACCATGGAGTGGGTTTCCAGAAAGCAGATAGTCTAAACCGT-AAAGGG 1438
DB 1384 CCGCCGTCACACCATGGAGTGGGTCACACCAAGTAGTGTCTAAACCCCTCGGGAGG 1443
QY 1439 GCGTTTCCACGCGGAGATTCAGACTGG 1467
DB 1444 ACCTTTACCACGGTGTGGTCAATGACTTG 1472

RESULT 8

US-10-659-980A-19
; Sequence 19, Application US/10659980A
; Publication No. US2004010613JA1
; GENERAL INFORMATION:
; APPLICANT: Hovanec, Timothy A
; TITLE OF INVENTION: Method for Detecting Ammonia-Oxidizing Bacteria
; FILE REFERENCE: 81289-284781
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: US/10/659,980A
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 60/386,217
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,218
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,219
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 1494
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: N. Aestuarii-like AOB P4clone31 16S rDNA
US-10-659-980A-19

Query Match 95.7%; Score 1403.4; DB 7; Length 1494;
Best Local Similarity 98.1%; Pred. No. 0;
Matches 1441; Conservative 0; Mismatches 26; Indels 2; Gaps 2;

QY 1 TTGATCATGGCTCAGATTGAACGCTGCGCGCATGCTTTACACATGCAAGTCGAACGCGCAG 60
DB 4 TTGATCATGGCTCAGATTGAACGCTGCGCGCATGCTTTACACATGCAAGTCGAACGCGCAG 63
QY 61 CACGGGTGCTTGACCTCGTGGCGAGTGGCGGACGGGTGAGTAATCATCGGAACGCTGTC 120
DB 64 CACGGGTGCTTGACCTCGTGGCGAGTGGCGGACGGGTGAGTAATCATCGGAACGCTGTC 123
QY 121 CAGAAAGTGGGGGATAACGCATCGAAAGATGCTAATACCGCATATTCTCTACGGAGGAA 180
DB 124 CGAAAGTGGGGGATAACGCATCGAAAGATGCTAATACCGCATATTCTCTACGGAGGAA 183
QY 181 AGCAGGGGATCGAAAGACCTTGCTTTTGAGCGCGCGATGCTCCTGATTAGCTAGTTGGT 240
DB 184 AGCAGGGGATCGAAAGACCTTGCTTTTGAGCGCGCGATGCTCCTGATTAGCTAGTTGGT 243
QY 241 GGGGTAAAGGCTTACCAAGGCAACGATCAGTAGTTGCTTGAGAGGACGACGAGCCACAC 300
DB 244 GGGGTAAAGGCTTACCAAGGCAACGATCAGTAGTTGCTTGAGAGGACGACGAGCCACAC 303
QY 301 TGGGACTGAGACACGGCCACATCTTACGGGAGGACGAGTGGGGAATTTTGGACAATG 360
DB 304 TGGGACTGAGACACGGCCACATCTTACGGGAGGACGAGTGGGGAATTTTGGACAATG 363
QY 361 GCGAAAGCCTGATCCAGCAATGCCGCTGAGTGAAGAAGG-CTTCGGGTTGTTAAAGCTC 419
DB 364 GCGAAAGCCTGATCCAGCAATGCCGCTGAGTGAAGAAGGCTTCGGGTTGTTAAAGCTC 423
QY 420 TTTGAGTCCGAGAGAAAGGTTGTGACTAATAATCACAACCTTATGATGGTACCGACGAA 479
DB 424 TTTGAGTCCGAGAGAAAGGTTGTGACTAATAATCACAACCTTATGATGGTACCGACGAA 483

QY 480 GAAGCACCGGCTAACTAGTGCACGACGCGGTAATACTAGTAGGTGCAAGCGTTAAATC 539
DB 484 GAAGCACCGGCTAACTAGTGCACGACGCGGTAATACTAGTAGGTGCAAGCGTTAAATC 543
QY 540 GGAATTTACTGGCGGTAAAGGGTGCACGACGCGCTTTTGAAGTCAGATGTGAATCCCCCG 599
DB 544 GGAATTTACTGGCGGTAAAGGGTGCACGACGCGCTTTTGAAGTCAGATGTGAATCCCCCG 603
QY 600 GCTTAACTGGGAATTCGTTTGAATCAACAAAGCTAGAGTGTAGCAGAGGGGGTGGAA 659
DB 604 GCTTAACTGGGAATTCGTTTGAATCAACAAAGCTAGAGTGTAGCAGAGGGGGTGGAA 663
QY 660 TTCCATGTGTAGCAGTGAATTCGATAGATATGAAGAAACATCGATGCGAAGGCGAGCC 719
DB 664 TTCCATGTGTAGCAGTGAATTCGATAGATATGAAGAAACATCGATGCGAAGGCGAGCC 723
QY 720 CCTCGGTTAACTAGCAGCTCATGCAAGAAAGCGTGGGAGCAAAACAGGATTAGATACC 779
DB 724 CCTCGGTTAACTAGCAGCTCATGCAAGAAAGCGTGGGAGCAAAACAGGATTAGATACC 783
QY 780 CTGGTAGTCACGCCCTAAACGATGTCACTAGTTGTTGGGCTTACTAGGCTTGTGTAAC 839
DB 784 CTGGTAGTCACGCCCTAAACGATGTCACTAGTTGTTGGGCTTACTAGGCTTGTGTAAC 843
QY 840 GTAGCTAAACGCGTGAAGTTGACCGCTGCGGAGTAGCGTTCGAGGATTAATACTCAAGG 899
DB 844 GTAGCTAAACGCGTGAAGTTGACCGCTGCGGAGTAGCGTTCGCAAGATTAATACTCAAGG 903
QY 900 AATTGACGGGGACCGGCACAAAGCGTGTGATTTAGTGGATTAATTCGATGCAAGCGCAAAA 959
DB 904 AATTGACGGGGACCGGCACAAAGCGTGTGATTTAGTGGATTAATTCGATGCAAGCGCAAAA 963
QY 960 ACCTTACCTACCTTACGATGTAGCGAATATTAGAGATAAAATAGTCTTCGCGAAC 1019
DB 964 ACCTTACCTACCTTACGATGTAGCGAATATTAGAGATAAAATAGTCTTCGCGAAC 1023
QY 1020 GCTAAACACAGGTGCTGATGGCTGCTGATGCTGCTGAGATGTTGGGTAAAGTCC 1079
DB 1024 GCTAAACACAGGTGCTGATGGCTGCTGATGCTGCTGAGATGTTGGGTAAAGTCC 1083
QY 1080 CGCAACGAGCGCAACCCCTTGTCAATTTGCCATCAATTTAGTTGGGACCTTTAATGAGAC 1139
DB 1084 CGCAACGAGCGCAACCCCTTGTCAATTTGCCATCAATTTAGTTGGGACCTTTAATGAGAC 1143
QY 1140 TGCCTGTGACAAACCGGAGAGGTGGGATGACGTCAAGTCTCTCATGGCCCTTATGGGT 1199
DB 1144 TGCCTGTGACAAACCGGAGAGGTGGGATGACGTCAAGTCTCTCATGGCCCTTATGGGT 1203
QY 1200 AGGGCTTTCACAGTAATACAAATGGCGGTACAGAGGGTTGCCAACCCCGAGGGGAGCT 1259
DB 1204 AGGGCTTTCACAGTAATACAAATGGCGGTACAGAGGGTTGCCAACCCCGAGGGGAGCT 1263
QY 1260 AATCTCAGAAAGCGCTGCTAGTCCGAGTCGGAGTCTGCAACTCGACTCCGCTGAAGTCGG 1319
DB 1264 AATCTCAGAAAGCGCTGCTAGTCCGAGTCGGAGTCTGCAACTCGACTCCGCTGAAGTCGG 1323
QY 1320 AATCGCTAGTAAATCGCGGATCAGCATGTGCGGTGAATACGTTTCCGGGTCTTTGTACACA 1379
DB 1324 AATCGCTAGTAAATCGCGGATCAGCATGTGCGGTGAATACGTTTCCGGGTCTTTGTACACA 1383
QY 1380 CCGCCCGTCACACCATGGGAGTGGTTTACCAAGAGCAGATAGTCTAACCGT-AAGAGG 1438
DB 1384 CCGCCCGTCACACCATGGGAGTGGTTTACCAAGAGCAGATAGTCTAACCGT-AAGAGG 1443
QY 1439 GCGTTTCCACGCGGAGATTCATGACTGG 1467
DB 1444 ACCTTACCACGGTGTGGTCAATGACTTG 1472

GENERAL INFORMATION: ;
APPLICANT: Hovanec, Timothy A ;
TITLE OF INVENTION: Ammonia-Oxidizing Bacteria ;
FILE REFERENCE: 81289-284779 ;
CURRENT APPLICATION NUMBER: US/10/659,983A ;
CURRENT FILING DATE: 2003-09-10 ;
PRIOR APPLICATION NUMBER: US 09/573,684 ;
PRIOR FILING DATE: 2000-05-19 ;
PRIOR APPLICATION NUMBER: US 60/386,217 ;
PRIOR FILING DATE: 2002-09-19 ;
PRIOR APPLICATION NUMBER: US 60/386,218 ;
PRIOR FILING DATE: 2002-09-19 ;
PRIOR APPLICATION NUMBER: US 60/386,219 ;
NUMBER OF SEQ ID NOS: 23 ;
SOFTWARE: PatentIn version 3.2 ;
SEQ ID NO 19 ;
LENGTH: 1494 ;
TYPE: DNA ;
ORGANISM: Unknown ;
FEATURE: ;
OTHER INFORMATION: N. Aestuarii-like AOB p4clone31 16S rDNA ;
US-10-659-983A-19 ;

Query Match 95.7%; Score 1403.4; DB 7; Length 1494;
Best Local Similarity 98.1%; Pred. No. 0;
Matches 1441; Conservative 0; Mismatches 26; Indels 2; Gaps 2;

Qy 1 TTGATCATGGCTCAGATTGAACGCTGGCGGATGCTTTACACATGCAAGTCGAACGGCAG 60
Db 4 TTGATCATGGCTCAGATTGAACGCTGGCGGATGCTTTACACATGCAAGTCGAACGGCAG 63

Qy 61 CACGGGTCTTGCACCTGGTGGCGAGTGGCGGAGTGGTGAATGATCGAAGCGTGC 120
Db 64 CACGGGTCTTGCACCTGGTGGCGAGTGGCGGAGTGGTGAATGATCGAAGCGTGC 123

Qy 121 CAGAAAGTGGGGATTAACGCATCGAAAGATGTCTAATACCGCATATCTCTACGAGGAA 180
Db 124 CGGAAGTGGGGATTAACGCATCGAAAGATGTCTAATACCGCATATCTCTACGAGGAA 183

Qy 181 AGCAGGGGATCGAAAGACCTTGTGCTTTTGAGCGCGCGATGCTGTAGTATTGTTGGT 240
Db 184 AGCAGGGGATCGAAAGACCTTGTGCTTTTGAGCGCGCGATGCTGTAGTATTGTTGGT 243

Qy 241 GGGGTAAAGGCTTACCAAGGCAACGATCAGTATTGTTGCTCAGAGGAGCAGCAGCCAC 300
Db 244 GGGGTAAAGGCTTACCAAGGCAACGATCAGTATTGTTGCTCAGAGGAGCAGCAGCCAC 303

Qy 301 TGGGACTGAGACACGGCCAGACTCTTACGGGAGCAGCAGTGGGGAATTTTGACAATG 360
Db 304 TGGGACTGAGACACGGCCAGACTCTTACGGGAGCAGCAGTGGGGAATTTTGACAATG 363

Qy 361 GCGGAAAGCCCTGATCCAGCAATCCGCGTGAGTGAAGAAGG-CTTCGGGTTGTAAAGCTC 419
Db 364 GCGGAAAGCCCTGATCCAGCAATCCGCGTGAGTGAAGAAGGCTTTCGGGTTGTAAAGCTC 423

Qy 420 TTTTCAGTCGAGAGAAAGGTTGTGACTAATAATCAACATTTATGATGTTACCGACAGAA 479
Db 424 TTTTCAGTCGAGAGAAAGGTTGTGACTAATAATCAACATTTATGATGTTACCGACAGAA 483

Qy 480 GAAGCAGCGGCTAACTAGTCCAGCAGCAGCGGCTAATACGTAGGCTGCAAGCGTTAATC 539
Db 484 GAAGCAGCGGCTAACTAGTCCAGCAGCAGCGGCTAATACGTAGGCTGCAAGCGTTAATC 543

Qy 540 GGAATTAATCGGCGTAAAGGTTGGCGAGCGGCTTTGTAAGTCAGATGTGAAATCCCGG 599
Db 544 GGAATTAATCGGCGTAAAGGTTGGCGAGCGGCTTTGTAAGTCAGATGTGAAATCCCGG 603

Qy 600 GCTTAACCTGGGAATTCGTTGAAACTACAAAGCTAGATGTAGCAGAGGGGGGTGAA 659
Db 604 GCTTAACCTGGGAATTCGTTGAAACTACAAAGCTAGATGTAGCAGAGGGGGGTGAA 663

Qy 660 TTCCATGTGTAGCAGTGAATGCGTGTAGAGATATGGAAGAACATCGATGCGGAGGCAGCC 719

Db 664 TTCCATGTGTAGCAGTGAATGCGTGTAGAGATATGGAAGAACATCGATGCGGAGGCAGCC 723

Qy 720 CCCTGGGTTTAAACATGACGCTCATGCAAGAAAGCGTGGGAGCAACAGGATTAGATACC 779

Db 724 CCCTGGGTTTAAACATGACGCTCATGCAAGAAAGCGTGGGAGCAACAGGATTAGATACC 783

Qy 780 CTGGTAGTCCACGCGCTTAAACGATGTCAACTAGTGTGTTGGGCTTACTAGGCTTCGTAAC 839

Db 784 CTGGTAGTCCACGCGCTTAAACGATGTCAACTAGTGTGTTGGGCTTACTAGGCTTCGTAAC 843

Qy 840 GTAGCTAAACGCGTGAAGTTGACCGCTTGGGAGTACGCTCGCAGGATTTAAACCTCAAGG 899

Db 844 GTAGCTAAACGCGTGAAGTTGACCGCTTGGGAGTACGCTCGCAGGATTTAAACCTCAAGG 903

Qy 900 AATTGACGGGGACCGGCACAAAGCGGTGGATTATGTGATTAATTCGATGCAACGCGAATA 959

Db 904 AATTGACGGGGACCGGCACAAAGCGGTGGATTATGTGATTAATTCGATGCAACGCGAATA 963

Qy 960 ACCTTACTACCTTTCATGACATGACGGAATATTTTAGAGATAAAATAGTGCCTTCGGGAAC 1019

Db 964 ACCTTACTACCTTTCATGACATGACGGAATATTTTAGAGATAAAATAGTGCCTTCGGGAAC 1023

Qy 1020 GCTTAACACAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1079

Db 1024 GCTTAACACAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1083

Qy 1080 CGCAACGAGGCGCAACCTTGTGCTAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1139

Db 1084 CGCAACGAGGCGCAACCTTGTGCTAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1143

Qy 1140 TGGCGGTGACAAACCGGAGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGT 1199

Db 1144 TGGCGGTGACAAACCGGAGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGT 1203

Qy 1200 AGGCTTTCACACGTAATACATGTCGCGGTACAGAGGGTTCGCAACCCGCGAGGGGGAGCT 1259

Db 1204 AGGCTTTCACACGTAATACATGTCGCGGTACAGAGGGTTCGCAACCCGCGAGGGGGAGCT 1263

Qy 1260 AATCTGAGAAAGCGCGTGTGATCCGGATCGGAGTTCGCAACTCGACTCCGCTGGAAGTCGG 1319

Db 1264 AATCTGAGAAAGCGCGTGTGATCCGGATCGGAGTTCGCAACTCGACTCCGCTGGAAGTCGG 1323

Qy 1320 AATCGCTAGTAATCGCGGATCAGCATGTGCGGTTGAATACGTTCCCGGCTTGTGACACA 1379

Db 1324 AATCGCTAGTAATCGCGGATCAGCATGTGCGGTTGAATACGTTCCCGGCTTGTGACACA 1383

Qy 1380 CCGCCCTCACACCATGCGGAGTGGGTTTCCACGAGGAGATAGTCTAAACCGT-AAGAGG 1438

Db 1384 CCGCCCTCACACCATGCGGAGTGGGTTTCCACGAGGAGATAGTCTAAACCGT-AAGAGG 1443

Qy 1439 GCGTTTCCACGCGGAGATTCATGACTGG 1467

Db 1444 ACGTTACCAACGCGTGTGCTCAATGACTTG 1472

RESULT 10
US-10-659-983A-1
; Sequence 1, Application US/10659948A
; Publication No. US20040101946A1
; GENERAL INFORMATION:
; APPLICANT: Hovanec, Timothy A
; TITLE OF INVENTION: Method of Using Ammonia-Oxidizing Bacteria
; FILE REFERENCE: 81289-294309
; CURRENT APPLICATION NUMBER: US/10/659,948A
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: US 09/573,684
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 60/386,217
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,218
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,219

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; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1457
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: AOB Type A R7clone140 16S rDNA
US-10-659-948A-1

Query Match          92.6%; Score 1358.8; DB 7; Length 1457;
Best Local Similarity 97.2%; Pred. No. 0;
Matches 1414; Conservative 0; Mismatches 37; Indels 3; Gaps 3;

QY 16 ATTGAACGCTGGCGGATGCTTTTACACATCGAAGTGAAGCGGAGCAGCGGTCTTGCAC 75
DB 1 ATTGAACGCTGGCGGATGCTTTTACACATCGAAGTGAAGCGGAGCAGCGGTCTTGCAT 60

QY 76 CTGGTGGCGAGTGGCGGACCGGTGAGTAATGCATCGGAACGTGTCCAGAAAGTGGGGATA 135
DB 61 CTGGTGGCGAGTGGCGGACCGGTGAGTAATGCATCGGAACGTGTCCAGAAAGTGGGGATA 120

QY 136 ACGCATCGAAAGATGTCTAATACCGCATATTCTTACGGAGGAAAGCAGCGGATCGAAA 195
DB 121 ACGCATCGAAAGATGTCTAATACCGCATATTCTTACGGAGGAAAGCAGCGGATCGAAA 180

QY 196 GACCTTGCTGCTTTGGAGCGCGCATGCTCTGATAGTGTAGTGTGGGGTAAAGGCTTAC 255
DB 181 GACCTTGCTGCTTTGGAGCGCGCATGCTCTGATAGTGTAGTGTGGGGTAAAGGCTTAC 240

QY 256 CAAGGCAACGATCAGTAGTGTGCTGAGAGGACGACCGACCACTGGGACTGAGACAG 315
DB 241 CAAGGCAACGATCAGTAGTGTGCTGAGAGGACGACCGACCACTGGGACTGAGACAG 300

QY 316 GCCCAGACTCTACGGAGGACGAGTGGGGAATTTTGGCAATGGGCGAAAGCTGATC 375
DB 301 GCCCAGACTCTACGGAGGACGAGTGGGGAATTTTGGCAATGGGCGAAAGCTGATC 360

QY 376 CAGCAATGCCGCTGAGTGAAGAAGG-CTTCGGGTTGTAAGCTCTTTTCAGTCGAGAAGA 434
DB 361 CAGCAATGCCGCTGAGTGAAGAAGGCTTCGGGTTGTAAGCTCTTTTCAGTCGAGAAGA 420

QY 435 AAAGGTTGTGACTAATATACACTTATATGATCGGACGAGGACGACCGGCTAAC 494
DB 421 AAAGGTTGTGACTAATATATGATCGGACGAGGACGACCGGCTAAC 480

QY 495 TAGCTGCCAGCAGCGCGGTAATACGTAGGCTGCAAGCGTTAATCGGAATTTACTGGGCGT 554
DB 481 TAGCTGCCAGCAGCGCGGTAATACGTAGGCTGCAAGCGTTAATCGGAATTTACTGGGCGT 540

QY 555 AAAGGTTGCCAGCGCGCTTTGTAAGTCAGATGTAATCCCGGCTTAACTGGGAAT 614
DB 541 AAAGGTTGCCAGCGCGCTTTGTAAGTCAGATGTAATCCCGGCTTAACTGGGAAT 600

QY 615 TGGCTTTGAACTCAAGCTAGAGTCTAGCAGAGGGGGTGGAAATCCCATGTGTACAG 674
DB 601 TGGCTTTGAACTCAAGAGCTAGAGTGTGGCAGAGGGAGGTGGAAATCCCATGTGTACAG 660

QY 675 TGAATTCGTAGAGATATGGAAGAACATCGATGCGAAGGCGAGCCCTCGGGTTAACT 734
DB 661 TGAATTCGTAGAGATATGGAAGAACATCGATGCGAAGGCGAGCCCTCGGGTTAACT 720

QY 735 GACGCTCATGCAAGAACGCTGGGAGCAACAGGATAGATACCTTGGTAGTCCAGCC 794
DB 721 GACGCTCATGCAAGAACGCTGGGAGCAACAGGATAGATACCTTGGTAGTCCAGCC 780

QY 795 CTAACGATGTCAACTAGTGTTCGGGCTTACTAGGCTTGTGATACGTAGCTAACCGCTGA 854
DB 781 CTAACGATGTCAACTAGTGTTCGGGCTTACTAGGCTTGTGATACGTAGCTAACCGCTGA 840

QY 855 AGTTGACCGCTGGGAGTACGGTCGACGAGGATTAATACTCAAGGAATTTGACGGGACCC 914
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DB 841 AGTTGACCGCTGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGACCC 900
QY 915 GCACAAGCGGTGATATATGATGATTAATTCGATGCAACCGGAAAAACCTTACCTACCTT 974
DB 901 GCACAAGCGGTGATATATGATGATTAATTCGATGCAACCGGAAAAACCTTACCTACCTT 960
QY 975 GACATGTAGCGAATATTTTAGAGATAAAATAGTGCCTTCGGGAACGCTAACACAGGTGCT 1034
DB 961 GACATGTAGCGAATATTTTAGAGATAAAATAGTGCCTTCGGGAACGCTAACACAGGTGCT 1019
QY 1035 GCATGGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1094
DB 1020 GCATGGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1079
QY 1095 CTTTGTCTAATTTGGCATCATTTAGTTGGGCACTTTTAATGAGACTGCCGCTGACAAACC 1154
DB 1080 CTTTGTCTAATTTGGCATCATTTAGTTGGGCACTTTTAATGAGACTGCCGCTGACAAACC 1139
QY 1155 GGAGGAAGGTGGGGATGAGTCAAGTCTCATGGCCCTTATGGGTAGGGCTTACACAGTA 1214
DB 1140 GGAGGAAGGTGGGGATGAGTCAAGTCTCATGGCCCTTATGGGTAGGGCTTACACAGTA 1199
QY 1215 ATACAAATGGCGGTACAGAGGGTTGCAACCCCGAGGGGAGCTAATCTCAGAAAGCGC 1274
DB 1200 ATACAAATGGCGGTACAGAGGGTTGCAACCCCGAGGGGAGCTAATCTCAGAAAGCGC 1259
QY 1275 GTCTGATGCTGGATCGGAGTCTGCAACTCGACTCCGCTGGAAGTCGGAATCGTAGTAACTG 1334
DB 1260 GTCTGATGCTGGATCGGAGTCTGCAACTCGACTCCGCTGGAAGTCGGAATCGTAGTAACTG 1319
QY 1335 CGGATCAGCATGTCGGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACACCA 1394
DB 1320 CGGATCAGCATGTCGGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACACCA 1379
QY 1395 TGGGAGTGGGTTTACCAAGAGCAGATAGTCTAACCCGTAA-GAGGGGTTTGGCAGCGCG 1453
DB 1380 TGGGAGTGGGTTTACCAAGAGCAGATAGTCTAACCCGTAAAGGAGGGCGCTTGGCAGCGTG 1439
QY 1454 AGATTCATGACTGG 1467
DB 1440 AGATTCATGACTGG 1453
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RESULT 11
US-10-659-980A-1
; Sequence 1, Application US/10659980A
; Publication No. US20040106133A1
; GENERAL INFORMATION:
; APPLICANT: Hovavsec, Timothy A
; TITLE OF INVENTION: Method for Detecting Ammonia-Oxidizing Bacteria
; FILE REFERENCE: 81289-284781
; CURRENT APPLICATION NUMBER: US/10/659,980A
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: US 09/573,684
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 60/386,217
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,218
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,219
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1457
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: AOB Type A R7clone140 16S rDNA
US-10-659-980A-1
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Query Match          92.6%; Score 1358.8; DB 7; Length 1457;
Best Local Similarity 97.2%; Pred. No. 0;
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Matches 1414; Conservative 0; Mismatches 37; Indels 3; Gaps 3;			
QY	16	ATTGAACGCTGCGGCATGCTTTACATGCAAGTCGAACGCGCAGCAGCGGTGCTTGAC	75
Db	1	ATTGAACGCTGCGGCATGCTTTACATGCAAGTCGAACGCGCAGCAGCGGTGCTTGAC	60
QY	76	CTGGTGGGAGTGGCGGACGGTGAGTAATGCGAAGTGGGGGATA	135
Db	61	CTGGTGGGAGTGGCGGACGGTGAGTAATGCGAAGTGGGGGATA	120
QY	136	ACGCATCGAAGATGCTAATACCGCATATTTCTACGGAGAAAGCAGGGGATCGAAA	195
Db	121	ACGCATCGAAGATGCTAATACCGCATATTTCTAAGGAGAAAGCAGGGGATCGAAA	180
QY	196	GACCTTGTGCTTTGGAGCGCGCATGCTGATTAAGTAGTGGTGGGTAAAGCCCTAC	255
Db	181	GACCTTGTGCTTTGGAGCGCGCATGCTGATTAAGTAGTGGTGGGTAAAGCCCTAC	240
QY	256	CAAGCCAAACGATCAGTAGTTGCTGAGAGGACGACCACTGGGACTTGAGACACG	315
Db	241	CAAGCCGACGATCAGTAGTTGCTGAGAGGACGACCACTGGGACTTGAGACACG	300
QY	316	GCCGAGCTCTACCGGAGGACGAGTGGGAAATTTTGGACAAATGGGCGAAAGCCTGATC	375
Db	301	GCCGAGCTCTCTACCGGAGGACGAGTGGGAAATTTTGGACAAATGGGCGCAAGCCTGATC	360
QY	376	CAGCAATCGCGCTGAGTGAAGAAGG-CCTCGGGTTGTAAAGCTCTTTCAGTCCGAGAGA	434
Db	361	CAGCAATCGCGCTGAGTGAAGAAGGCTTTCGGTTGTAAAGCTCTTTCAGTCCGAGAGA	420
QY	435	AAAGGTTGTGACTAATAATCAACCTTATGATGTGACCGACAGAAAGACCGGCTAAC	494
Db	421	AAAGGTTACGCTAATAATATCGTACTCATGCGGTATCGACAGAGAGACCGGCTAAC	480
QY	495	TACGTGCCAGCAGCGCGGTAAATACGTAGGGTGAAGCGTTAATCGGAATTACTGGGCGT	554
Db	481	TACGTGCCAGCAGCGCGGTAAATACGTAGGGTGAAGCGTTAATCGGAATTACTGGGCGT	540
QY	555	AAAGGTCGCGAGCGGCTTTGTAGTCAGATGTCGAATCCCGGCTTAACTCTGGGAT	614
Db	541	AAAGGTCGCGAGCGGCTTTGTAGTCAGATGTCGAATCCCGGCTTAACTCTGGGAT	600
QY	615	TGCGTTTGAACACTACAAAGCTAGAGTGTAGCAGAGGGGGTGGAAATTCATGTGTAGCAG	674
Db	601	TGCGTTTGAACACTACAAAGCTAGAGTGTGSCAGAGGGAGTGGAAATTCATGTGTAGCAG	660
QY	675	TGAATGCGTAGAGATATGGAAGAACATCGATGCGAAGGCGGCCCTCTGGGTAAACT	734
Db	661	TGAATGCGTAGAGATATGGAAGAACATCGATGCGAAGGCGGCCCTCTGGGTAAACT	720
QY	735	GACGCTCATGCAGAAAGCGTGGGAGCAACAGAGATTTAGATACCCTGGTAGTCCAGCC	794
Db	721	GACGCTCATGCAGAAAGCGTGGGAGCAACAGAGATTTAGATACCCTGGTAGTCCAGCC	780
QY	795	CTAAACGATGTCAACTAGTGTGGGCTTACTAGGCTTGGTAAGCTAGCTAACCGCTGA	854
Db	781	CTAAACGATGTCAACTAGTGTGGGCTTATAGGCTTGGTAAGCTAGCTAACCGCTGA	840
QY	855	AGTTGACCGCTGGGAGTACGGTCCGAGGATTAATACTCAAGGAATTTGACGGGACCC	914
Db	841	AGTTGACCGCTGGGAGTACGGTCCGAGGATTAATACTCAAGGAATTTGACGGGACCC	900
QY	915	GCACAGCGGTGGATATGCTGAATTAATTCGATGCAACGCGAATAACCTTACCTTACCCCTT	974
Db	901	GCACAGCGGTGGATATGCTGAATTAATTCGATGCAACGCGAATAACCTTACCTTACCCCTT	960
QY	975	GACATGTACGAATATTTTAGAGATAAAATAGTGCCTTTCGGGAAGCTTAAACACAGGTGCT	1034
Db	961	GACATGTACGAATATTTCTAGAGATAGATTAGTGC-TTCGGGAAGCTTAAACACAGGTGCT	1019
QY	1035	GATGGCTGTGCTCAGCTCGTGTGAGATGTTGGGTAAAGTCCCGCAACGAGCGCAAC	1094
Db	1020	GATGGCTGTGCTCAGCTCGTGTGAGATGTTGGGTAAAGTCCCGCAACGAGCGCAAC	1079

QY	1095	CCTGTCTAATTAATTCGCCATCATTTAGTTGGGCACCTTTAATGAGACTGCCGGTGACAAACC	1154
Db	1080	CCTGTCTAATTAATTCGCCATCATTTGGTTGGGCACCTTTAATGAGACTGCCGGTGACAAACC	1139
QY	1155	GGAGGAAGGTGGGGATGACGTCAGTCACTCTCATGGCCCTTATGGGTAGGCTTTACACGTA	1214
Db	1140	GGAGGAAGGTGGGGATGACGTCAGTCACTCTCATGGCCCTTATGGGTAGGCTTTACACGTA	1199
QY	1215	ATACATCGCGGCTACAGAGGTTGCCAAACCGCGAGGGGGAGCTAATCTCAGAAAGCGC	1274
Db	1200	ATACATCGCGGCTACAGAGGTTGCCAAACCGCGAGGGGGAGCTAATCTCAGAAAGCGC	1259
QY	1275	GTCTGTAGTCCGATCGGAGTCTCGAACTCGACTCGTCTGAAAGTCGGAATCGCTAGTAATCG	1334
Db	1260	GTCTGTAGTCCGATCGGAGTCTCGAACTCGACTCGTCTGAAAGTCGGAATCGCTAGTAATCG	1319
QY	1335	CGGATCAGCATGTCCGGTGAATAGCTTCCGGGTCTTTGTACACACCGCCCGTCCACCA	1394
Db	1320	CGGATCAGCATGTCCGGTGAATAGCTTCCGGGTCTTTGTACACACCGCCCGTCCACCA	1379
QY	1395	TGGAGTGGGTTTCCACGAGAGCAGATAGTCTAACCGTAA-GAGGGCGTTTCCACCGCG	1453
Db	1380	TGGAGTGGGTTTCCACGAGAGCAGTGTCTTAACCGTAAAGGAGGCGCTTCCACCGGTG	1439
QY	1454	AGATTTCATGACTGG	1467
Db	1440	AGATTTCATGACTGG	1453

RESULT 12

US-10-659-983A-1
; Sequence 1, Application US/10659983A
; Publication No. US20040157313A1
; GENERAL INFORMATION:
; APPLICANT: Hovanec, Timothy A
; TITLE OF INVENTION: Ammonia-Oxidizing Bacteria
; FILE REFERENCE: 81289-284779
; CURRENT APPLICATION NUMBER: US/10/659,983A
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: US 09/573,684
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 60/386,217
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,218
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,219
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1457
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: AOB Type A R7clone140 16S rDNA
US-10-659-983A-1

Query Match 92.6%; Score 1358.8; DB 7; Length 1457; Best Local Similarity 97.2%; Pred. No. 0; Matches 1414; Conservative 0; Mismatches 37; Indels 3; Gaps 3;			
QY	16	ATTGAACGCTGCGGCATGCTTTACATGCAAGTCGAACGCGCAGCAGCGGTGCTTGAC	75
Db	1	ATTGAACGCTGCGGCATGCTTTACATGCAAGTCGAACGCGCAGCAGCGGTGCTTGAC	60
QY	76	CTGGTGGGAGTGGCGGACGGTGAGTAATGCGAAGTGGGGGATA	135
Db	61	CTGGTGGGAGTGGCGGACGGTGAGTAATGCGAAGTGGGGGATA	120
QY	136	ACGCATCGAAGATGCTAATACCGCATATTTCTACGGAGGAAAGCAGGGGATCGAAA	195
Db	121	ACGCATCGAAGATGCTAATACCGCATATTTCTAAGGAGGAAAGCAGGGGATCGAAA	180

Qy	196	GACCTTGTGCTTTTGGAGCGCGCGATGCCCTGATTAGCTAGTTGGTGGGTAAAGGCTTAC	255
Db	181	GACCTTGGCTTTTGGAGCGCGCGATGTCGTGATTTAGCTAGTTGGTGGGTAAAGGCTTAC	240
Qy	256	CAAGGCAACCATCAGTAGTTGGTCTGAGAGGACGACCGACACCTCGGAGCTGAGACACG	315
Db	241	CAAGGCGACCATCAGTAGTTGGTCTGAGAGGACGACCGACACCTCGGAGCTGAGACACG	300
Qy	316	GCCCAGACTCCTACGGGAGCAGCAGTGGGGAATTTTGGACAAATGGGCGAAGCCCTGATC	375
Db	301	GCCCAGACTCCTACGGGAGCAGCAGTGGGGAATTTTGGACAAATGGGCGCAAGCCCTGATC	360
Qy	376	CAGCAATGCCCGCTGAGTGAAGAGG-CTTCGGGTGTAAAGCTCTTCAGTCGAGAAAGA	434
Db	361	CAGCAATGCCCGCTGAGTGAAGAGGCTTCGGGTGTAAAGCTCTTCAGTCGAGAAAGA	420
Qy	435	AAAGGTTGTGACTAATAATCACAACTTATGATGGTACCGACAGAAGAAGCACCGGCTAAC	494
Db	421	AAAGGTTTACGGTAAATAATCTGTGACTCATGACGGTATCGACAGAAGAAGCACCGGCTAAC	480
Qy	495	TACGTGCAGCAGCGCGGTAATACGTAGGGTGCACGGTTAATCGGAATTACTGGGCGT	554
Db	481	TACGTGCAGCAGCGCGGTAATACGTAGGGTGCACGGTTAATCGGAATTACTGGGCGT	540
Qy	555	AAAGGTCGCGAGCGGCTTTGTAAGTCAGATGTGAATCCCGGGCTTAACCTGGGAAT	614
Db	541	AAAGGTCGCGAGCGGCTTTGTAAGTCAGATGTGAATCCCGGGCTTAACCTGGGAAT	600
Qy	615	TGCGTTTGAATCTACAAAGCTAGAGTGTAGCAGAGGGGGTGGAAATCCATGTGTAGCAG	674
Db	601	TGCGTTTGAATCTACAAAGCTAGAGTGTAGCAGAGGGGGTGGAAATCCATGTGTAGCAG	660
Qy	675	TGAATGCGTAGAGTATGGAAGACATCGATGCGAAGGCGAGCCCTCGGTAAACACT	734
Db	661	TGAATGCGTAGAGTATGGAAGACATCGATGCGAAGGCGAGCCCTCGGTAAACACT	720
Qy	735	GACGCTCATGCACGAAACGCTGGGAGCAAA CAGGATTTAGATACCTCGGTAGTCCAGCC	794
Db	721	GACGCTCATGCACGAAACGCTGGGAGCAAA CAGGATTTAGATACCTCGGTAGTCCAGCC	780
Qy	795	CTAAACGATGTCAACTAGTTGTTGGCCCTTACTAGGCTTGATAGCTTAACGCTGA	854
Db	781	CTAAACGATGTCAACTAGTTGTTGGCCCTTACTAGGCTTGATAGCTTAACGCTGA	840
Qy	855	AGTTGACCCCTTGGGAGTACGCTCGCAGGATTTAAACTCAAAGGAATTTGACGGGACCC	914
Db	841	AGTTGACCCCTTGGGAGTACGCTCGCAGGATTTAAACTCAAAGGAATTTGACGGGACCC	900
Qy	915	GCACAAGCGGTGGATTTATGTGATTAATTCGATGCAACGCGAANAACCTTACCTACCCCT	974
Db	901	GCACAAGCGGTGGATTTATGTGATTAATTCGATGCAACGCGAANAACCTTACCTACCCCT	960
Qy	975	GACATGTACGAAATTTTAGAGATAAATAGTGCCTTCGGAGCGCTTAACACAGGTGCT	1034
Db	961	GACATGTACGAAATTTTCTAGAGATAGATTAGTGC- TTCCGGNAACGCTTAA CACAGTGTCT	1019
Qy	1035	GCATGCTGTGCTGACGCTGCTGCTGAGATGTTGGGTTAAGTCCGCAAGAGCGCAAC	1094
Db	1020	GCATGCTGTGCTGACGCTGCTGCTGAGATGTTGGGTTAAGTCCGCAAGAGCGCAAC	1079
Qy	1095	CCTTGTCAATTAATTTGCGCATTTAGTTGGGCACCTTAAATGAGACTTGGCGGTGACAAACC	1154
Db	1080	CCTTGTCAATTAATTTGCGCATTTAGTTGGGCACCTTAAATGAGACTTGGCGGTGACAAACC	1139
Qy	1155	GGAGGAAGGTGGGATGACGTCAAGTCTCATGGGCCCTTATGGGTAGGCTTCAACGTA	1214
Db	1140	GGAGGAAGGTGGGATGACGTCAAGTCTCATGGGCCCTTATGGGTAGGCTTCAACGTA	1199
Qy	1215	ATACAAATGGCGGTTACAGAGGGTTGCCAACCCCGAGGGGAGCTTAATCTCAGAAAGCGC	1274
Db	1200	ATACAAATGGCGGTTACAGAGGGTTGCCAACCCCGAGGGGAGCTTAATCTCAGAAAGCGC	1259
Qy	1275	GTCGTAGTCCGGATCGAGTCTGCAACTCGACTCCGTGAAGTCCGAATCGCTAGTAATCG	1334
Db	1260	GTCGTAGTCCGGATCGAGTCTGCAACTCGACTCCGTGAAGTCCGAATCGCTAGTAATCG	1319
Qy	1335	CGGATCAGATGTCGGGTGAATACGTTCCCGGTCTTTGTACACACCGCCCGTCAACACCA	1394
Db	1320	CGGATCAGATGTCGGGTGAATACGTTCCCGGTCTTTGTACACACCGCCCGTCAACACCA	1379
Qy	1395	TGGGAGTGGGTTTCCACAGAACGAGATAGTCTAACCGTAA- GAGGGGCTTTGCCACGGCG	1453
Db	1380	TGGGAGTGGGTTTCCACAGAACGAGTAGTCTAACCGTAAAGGAGGGCGCTTTGCCACGGTG	1439
Qy	1454	AGATTTCATGACTGG 1467	
Db	1440	AGATTTCATGACTGG 1453	
RESULT 13			
US-10-659-948A-2			
; Sequence 2, Application US/10659948A			
; Publication No. US20040101946A1			
; GENERAL INFORMATION:			
; APPLICANT: Hovanec, Timothy A			
; TITLE OF INVENTION: Method of Using Ammonia-Oxidizing Bacteria			
; FILE REFERENCE: 81289-294309			
; CURRENT APPLICATION NUMBER: US/10/659,948A			
; CURRENT FILING DATE: 2003-09-10			
; PRIOR APPLICATION NUMBER: US 09/573,684			
; PRIOR FILING DATE: 2000-05-19			
; PRIOR APPLICATION NUMBER: US 60/386,217			
; PRIOR FILING DATE: 2002-09-19			
; PRIOR APPLICATION NUMBER: US 60/386,218			
; PRIOR FILING DATE: 2002-09-19			
; PRIOR APPLICATION NUMBER: US 60/386,219			
; PRIOR FILING DATE: 2002-09-19			
; NUMBER OF SEQ ID NOS: 23			
; SOFTWARE: PatentIn version 3.2			
; SEQ ID NO 2			
; LENGTH: 1457			
; TYPE: DNA			
; ORGANISM: Unknown			
; FEATURE:			
; OTHER INFORMATION: AOB Type A1 R7clone187 16S rDNA			
US-10-659-948A-2			
Query Match 92.5%; Score 1357.2; DB 7; Length 1457;			
Best Local Similarity 97.2%; Pred. No. 0;			
Matches 1413; Conservative 0; Mismatches 38; Indels 3; Gaps 3;			
Qy	16	ATTGAACGCTGGCGGCATGCTTTACATGCAAGTCAAGCGGAGCAGCGGTCCTTGCAC	75
Db	1	ATTGAACGCTGGCGGCATGCTTTACATGCAAGTCAAGCGGAGCAGCGGTCCTTGCAT	60
Qy	76	CTGGTGGCGAGTGGCGGCGGGTGAATGCAATCGAACTGTCAGAAAGTGGGGGATA	135
Db	61	CTGGTGGCGAGTGGCGGCGGGTGAATGCAATCGAACTGTCAGAAAGTGGGGGATA	120
Qy	136	ACGCATCGAAAGATGTCTAATACCCGCATATTTCTCTACGGAGGAAAGCGGGGATGAAA	195
Db	121	ACGCATCGAAAGATGTCTAATACCCGCATATTTCTAAGGAGGAAAGCGGGGATGAAA	180
Qy	196	GACCTTGTCTTTTGGAGCGCGCGATGCTGATTTAGTCTAGTTGGGTAAAGGCTTAC	255
Db	181	GACCTTGTCTTTTGGAGCGCGCGATGCTGATTTAGTCTAGTTGGGTAAAGGCTTAC	240
Qy	256	CAAGGCAACCATCAGTAGTTGGTCTGAGAGGACGACCGACACCTGGGACTGAGACACG	315
Db	241	CAAGGCAACCATCAGTAGTTGGTCTGAGAGGACGACCGACACCTGGGACTGAGACACG	300
Qy	316	GCCCAGACTCCTACGGGAGCAGCAGTGGGGAATTTTGGCAATGGCGGAAGCCTGATC	375
Db	301	GCCCAGACTCCTACGGGAGCAGCAGTGGGGAATTTTGGCAATGGCGGAAGCCTGATC	360

376 CAGCAATGCCGCTGAGTGAAGAAGG-CTTCGGGTTGTAAAGCTCTTTCACTCGAGAAGA 434
Db |||||
361 CAGCAATGCCGCTGAGTGAAGAAGGCTTTCGGGTTGTAAAGCTCTTTCACTCGAGAAGA 420
Qy |||||
435 AAAGGTTGTGACTAATATCAACTTATGATGTTACCGACAGAAGAAGCACCGGCTTAAC 494
Db |||||
421 AAAGGTTACGGTAAATATCTGTGACCCATGACGGTATCGACAGAAGAAGCACCGGCTAAC 480
Qy |||||
495 TACGTGCCAGCAGCGCGGTAACTAGTGGGTGCAAGCGTTAAATCGGAATTAATCTGGCGGT 554
Db |||||
481 TACGTGCCAGCAGCGCGGTAACTAGTGGGTGCAAGCGTTAAATCGGAATTAATCTGGCGGT 540
Qy |||||
555 AAAGGTTGCCAGCGCGCTTGTAAAGTCAGATGTGAATCCCGGGCTTAACCTGGGAAT 614
Db |||||
541 AAAGGTTGCCAGCGCGCTTGTAAAGTCAGATGTGAATCCCGGGCTTAACCTGGGAAT 600
Qy |||||
615 TGCCTTTGAAACTCAAAAGCTAGAGTGTAGCAGAGGGGGTGGAAATTCATGTGTAGCAG 674
Db |||||
601 TGCCTTTGAAACTCAAAAGCTAGAGTGTAGCAGAGGGGGTGGAAATTCATGTGTAGCAG 660
Qy |||||
675 TGAATGCTAGAGATATGGAAGACATCGATGCGGAGGCGAGCCCTGGGTTAACTACT 734
Db |||||
661 TGAATGCTAGAGATATGGAAGACATCGATGCGGAGGCGAGCCCTGGGTTAACTACT 720
Qy |||||
735 GACGCTCATGCAAGGAGCGTGGGAGCAAAACAGGATTAGATACCTGGTGTACAGGCC 794
Db |||||
721 GACGCTCATGCAAGGAGCGTGGGAGCAAAACAGGATTAGATACCTGGTGTACAGGCC 780
Qy |||||
795 CTAACAGATGTCAACTAGTTGTTGGGCTTACTAGGCTTGTAACGTAGCTTAACCGGTGA 854
Db |||||
781 CTAACAGATGTCAACTAGTTGTTGGGCTTACTAGGCTTGTAACGTAGCTTAACCGGTGA 840
Qy |||||
855 AGTTGACCGCTGCGGAGTACGGTCCGAGGATTAATACTCAAGGATTGACGGGAGCC 914
Db |||||
841 AGTTGACCGCTGCGGAGTACGGTCCGAGGATTAATACTCAAGGATTGACGGGAGCC 900
Qy |||||
915 GCACAAGCGGTGGATTATGTGGATTAAATTCGATGCAAGCGCAAAAACCTTACCTACCTT 974
Db |||||
901 GCACAAGCGGTGGATTATGTGGATTAAATTCGATGCAAGCGCAAAAACCTTACCTACCTT 960
Qy |||||
975 GACATGTAGCGAATPATTTTAGAGATAAATAAGTCCCTTCGGGAACGCTTAAACAGAGTGCT 1034
Db |||||
961 GACATGTAGCGAATPATTTTAGAGATAGATTAGTGC-TTCGGGAACGCTTAAACAGAGTGCT 1019
Qy |||||
1035 GCATGCTGTGCTGAGTCTGCTGATGATGTTGGGTTAGTCCCGAAGCAGCGCAAC 1094
Db |||||
1020 GCATGCTGTGCTGAGTCTGCTGATGATGTTGGGTTAGTCCCGAAGCAGCGCAAC 1079
Qy |||||
1095 CTTTGTCAATTAATTTGCCATCAATTTAGTTGGGCACTTTTAATGAGACTGCGGTGACAAAC 1154
Db |||||
1080 CTTTGTCAATTAATTTGCCATCAATTTAGTTGGGCACTTTTAATGAGACTGCGGTGACAAAC 1139
Qy |||||
1155 GGAGGAAGGTGGGATGACGTCAAGTCTCATGCGCCCTTATGGGTAGGGCTTTCACAGTA 1214
Db |||||
1140 GGAGGAAGGTGGGATGACGTCAAGTCTCATGCGCCCTTATGGGTAGGGCTTTCACAGTA 1199
Qy |||||
1215 ATACAATGGCGGTACAGAGGGTTGCCAACCCCGAGAGGGGAGCTAATCTCAGAAAGGCG 1274
Db |||||
1200 ATACAATGGCGGTACAGAGGGTTGCCAACCCCGAGAGGGGAGCTAATCTCAGAAAGGCG 1259
Qy |||||
1275 GTCGTAGTCCGGATCGGAGTCTGCAACTCGACTCCGTGAACTCGGAATCGCTAGTAATCG 1334
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1260 GTCGTAGTCCGGATCGGAGTCTGCAACTCGACTCCGTGAACTCGGAATCGCTAGTAATCG 1319
Qy |||||
1335 CGGATCAGCATGTCCGCGTGAATACGTTCCCGGTCTTTGTACACACCGCCCGTTCACACCA 1394
Db |||||
1320 CGGATCAGCATGTCCGCGTGAATACGTTCCCGGTCTTTGTACACACCGCCCGTTCACACCA 1379
Qy |||||
1395 TGGAGTGGGTTTACCAAGAGCAGATAGTCTAACCGTAA-GAGGGGGTTTGCCACGGCG 1453
Db |||||
1380 TGGAGTGGGTTTACCAAGAGCAGATAGTCTAACCGGTAAAGGAGGGGGCTTTGCCACGGTG 1439
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1454 AGATTATGACTGG 1467

Db |||||
1440 AGATTATGACTGG 1453

RESULT 14

US-10-659-980A-2
; Sequence 2, Application US/10659980A
; Publication No. US20040106133A1
; GENERAL INFORMATION:
; APPLICANT: Hovanec, Timothy A
; TITLE OF INVENTION: Method for Detecting Ammonia-Oxidizing Bacteria
; FILE REFERENCE: 81289-284781
; CURRENT APPLICATION NUMBER: US/10/659,980A
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: US 09/573,684
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 60/386,217
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,218
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,219
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 1457
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: AOB Type A1 R7clone187 16S rDNA
US-10-659-980A-2

Query Match 92.5%; Score 1357.2; DB 7; Length 1457;
Best Local Similarity 97.2%; Pred. No. 0;
Matches 1413; Conservative 0; Mismatches 38; Indels 3; Gaps 3;
Qy 16 ATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACGCGACGACGGTGTCTTGAC 75
Db |||||
1 ATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACGCGACGACGGTGTCTTGAC 60
Qy 76 CTGTGTCGAGTGGCGGACGGGTGAGTAATGTCATCGGAACGTCGACAGAAATGGGGGATA 135
Db |||||
61 CTGTGTCGAGTGGCGGACGGGTGAGTAATGTCATCGGAACGTCGACAGAAATGGGGGATA 120
Qy 136 ACGCATCGAAGATGTCTTAATACCGCATATTTCTACGAGGAGGAAGCAGGGGATCGAAA 195
Db |||||
121 ACGCATCGAAGATGTCTTAATACCGCATATTTCTAAGGAGGAAAGCAGGGGATCGAAA 180
Qy 196 GACCTTGTCTTTGGAGCGCGCATGCTGATAGCTAGTTGGTGGGTAAAGCCCTAC 255
Db |||||
181 GACCTTGTCTTTGGAGCGCGCATGCTGATAGCTAGTTGGTGGGTAAAGCCCTAC 240
Qy 256 CAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCGCACACTGGGACTGAGACACG 315
Db |||||
241 CAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCGCACACTGGGACTGAGACACG 300
Qy 316 GCCCAGACTCCTACGGAGGACGAGTGGGGAATTTTGGCAATGGGGGAAGCCTGATC 375
Db |||||
301 GCCCAGACTCCTACGGAGGACGAGTGGGGAATTTTGGCAATGGGGGAAGCCTGATC 360
Qy 376 CAGCAATGCGCGGTGAGTGAAGAAGG-CTTCGGGTGTAAAGCTCTTTCACTCGAGAAGA 434
Db |||||
361 CAGCAATGCGCGGTGAGTGAAGAAGGCTTCGGGTGTAAAGCTCTTTCACTCGAGAAGA 420
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Db |||||
421 AAAGGTTGTGACTAATTAATCAACTTATGATGTTACCGACAGAAGAAGCACCGGCTTAAC 480
Qy 495 TACGTGCCAGCAGCGCGGTAAATACGTAGGGTGAAGGTTAATCGGATTAATCTGGGCGT 554
Db |||||
481 TACGTGCCAGCAGCGCGGTAAATACGTAGGGTGAAGGTTAATCGGATTAATCTGGGCGT 540
Qy 555 AAAGGTTGCCAGCGCGCTTTGTAAAGTCAGATGTGAATCCCGGGCTTTAACTCGGGAAT 614

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|||||
615 TGGGTTTGAACCTACAAAGCTAGAGTGTAGCAGAGGGGGTGAATTCATGTGTAGCAG 674
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; APPLICANT: Hovanec, Timothy A
; TITLE OF INVENTION: Ammonia-Oxidizing Bacteria
; FILE REFERENCE: 81289-284779
; CURRENT APPLICATION NUMBER: US/10/659,983A

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; CURRENT FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: US 09/573,684  
; PRIOR FILING DATE: 2000-05-19  
; PRIOR APPLICATION NUMBER: US 60/386,217  
; PRIOR FILING DATE: 2002-09-19  
; PRIOR APPLICATION NUMBER: US 60/386,218  
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Job time : 1289 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 6, 2006, 19:18:42 ; Search time 6253 Seconds
(without alignments)
10976.595 Million cell updates/sec

Title: US-10-659-983A-18

Perfect score: 1467

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: gb_est2.*
- 3: gb_est3.*
- 4: gb_est4.*
- 5: gb_est5.*
- 6: gb_est6.*
- 7: gb_est7.*
- 8: gb_est8.*
- 9: gb_est9.*
- 10: gb_est10.*
- 11: gb_est11.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	635	43.3	1084	9 B2439740	B2439740 BONDUS4TF
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6	625.2	42.6	1053	9 B2447500	B2447500 BONKFA0TR
7	621.4	42.4	1010	9 B2431523	B2431523 BONHDB8TF
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9	616.6	42.0	1051	9 B2494182	B2494182 BONHR54TR
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12	613.2	41.8	1079	9 BH705272	BH705272 BONKA47TF
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14	611.6	41.7	1077	9 B2450751	B2450751 BONBQ63TR
15	610	41.6	884	7 CK280528	CK280528 EST743250
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18	580.6	39.6	974	9 B2440868	B2440868 BONKTS1TR
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VERSION BH771024.1
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AUTHORS Bolotin,A., Ehrlich,S.D. and Sorokin,A.
TITLE Studies of genomes of dairy bacteria Lactococcus lactis
JOURNAL Sci. Alimentis (2002) In press
COMMENT Contact: Sorokin A
Genetique Microbienne
INRA
CRJ INRA, Domaine de Vilvert, 78352 Jouy en Josas cedex, France
Tel: 33 1 34 65 25 16
Fax: 33 1 34 65 25 21
Email: sorokin@jouy.inra.fr
Best homologue in strain IL1403 is ywga (78%)
Class: Shotgun
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SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
COMMENT

CX109203 1954 bp mRNA linear EST 03-JUN-2005
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Oryza sativa (indica cultivar-group)
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1 (bases 1 to 1954)
Zhang, J., Feng, Q., Jin, C., Qiu, D., Zhang, L., Xie, K., Yuan, D., Han, B., Zhang, Q. and Wang, S.
Features of the expressed sequences revealed by a large-scale analysis of ESTs from a normalized cDNA library of the elite indica rice cultivar Minghui 63
Plant J. 42 (5), 772-780 (2005)
1591889
Contact: Wang S
National Key Laboratory of Crop Genetic Improvement
Hauzhong Agricultural University
Wuhan 430070, China
Tel: 86-27-87282044
Fax: 86-27-87287092
Email: shenpingwang@hotmail.com
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ORIGIN

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Qy 1 TTGATCATGGCTCAGATTGAACGCTGGCGGCGATGCTTTACACATGCAAGTCAACGCGAG 60
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
113 TCGATCTCGCTCAGGATGAACGCTGGCGGCGATGCTTTAAACATGCAAGTCAACGCGAA 172
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
61 CACGGGTGCTTGACCTGGTGGCGAGTGGCGGAGCGGTGAGTAATGATCGGAACGTGTC 120
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
173 GTGGTGTT-----CAGTGGCGAAACGGGTGAGTAACGGGTGAACGCAACCTGCC 219
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
121 CAGAAGTGGGGGATAACGCATCGAAAGATGTCTAAATACCGCATATTTCTTACGGAGAA 180
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
220 CTTGGAGGGGAAACAACTGGAACGGTTGCTTAATACCCGTAGGCT----- 268
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
181 AGCAGGGGATCGAAGACCTTGTGCTTTGGAGCGCGCATGCTGATTTAGCTAGTTGTT 240
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
269 --GAGGAGCAAAAGAGAAATCCGCCAAGGAGGGGCTCGGCTCTGATTAGCTAGTTGGT 326
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
241 GGGTAAGGCTTACCAAGGCAACGATCAGTAGTTGTTCTGAGAGGAGGACGACGACAC 300
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
327 GAGCAATAGCTTACCAAGGCGATGATCAGTAGTTGTTCTGAGAGGAGGATGATCAGCCAC 386
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
301 TGGGACTGAGACACGGCCGACCTCTACGGGAGGCGAGCAGTGGGGAATTTTGACAAATG 360
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
387 TGGGACTGAGACACGGCCGACCTCTACGGGAGGCGAGCAGTGGGGAATTTTGCGCAATG 446
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
361 GCGGAAGCCTGATCCAGCAATCCGCGTGTAGTGAAGAAGG-CTTCGCGTTGTAAAGCTC 419
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
447 GCGGAAGCCTGACGGAGCAATCCGCGTGTAGTGTGAAGGCCCAACGGGTGCTCAATTC 506
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
420 TTTTCAGTCGAGAAAGGTTGTGACTAATAATCACAACATTTATGATGGTTACCAAGAA 479
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
507 TTTTCTCGGAGAGAA-----CAATGACGGTATCTGAGAA 543
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
480 GAAGCACCCTTAACCTAGCTGCCAGCAGCCGCGTAAATACCTAGGCTGCAAGCGTTAATC 539
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
544 TAAGCATCGGCTAATCTGTGTCAGAGCAGCCGCTAGACAGAGATGCAAGCGTTATCC 603
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
540 GGAATTAATCTGGCGTAAAGGCTGCGCAGCGGCTTTGTAAGTCAGATGTGAAATCCCGG 599
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
604 GGAATGATTGGCGTAAAGCGTCTGTAGTGGCTTTTCAAGTCCGCGTCAAAATCCCAAG 663
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
600 GCTTAACCTGGGAATTCGTTTGAACCTAACAAGCTAGATGTAGCAGAGGGGGTGGAA 659
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
664 GCTCAACCTGGACAGCGCGTGGAACTCAACAAGCTGGAGTACGTTAGGGGCGAGAGGAA 723
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
660 TTCCATGTGTAGCAGTGAATTCGTAGAGATATGGAAGCAATCGATGGCGGAAGCGAGCC 719
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
724 TTTCCGTTGAGCGGTGAATTCGATGAGATCGGAAGAACCAACCGCGGAAGCACTC 783
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
720 CCCTGGGTTAACTAGCAGCTCATCGCAAGAGCGTGGGAGCAAAACAGGATTAGATACC 779
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
784 TGCTGGGCGGACACTGACACTGAGAGACGAAAGCTAGGGGAGCAATGGGATTAGAGACC 843
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
780 CTGG--TAGTCCAGCCCTAAACATGTCACACTAGTGTGTTGGGCTTACTAGGCTTG--G 835
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
844 CCAGATAATCCATAGCCGTTAAACATGATAGTACTAGTGTCTGTGGGACTCGACCCGTCG 903
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
836 TAAAGTGTAGTAAACGCTGAAGTTGACCCCTCGGGGAGTACGCTGCGAGGATTTAAACTCA 895
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
904 TGCTGTAGTAAACGCTTAAAGTATCTCCGCTCGGGAGTACGTTTCGAGAGATGAAGACTCA 963
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
896 AAGGAATTCAGGGGACCCGACAAAGCGGTGGATTATGTGATTAATTCGATGCAAGCGG 955
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
964 AAGGAATTGACGGGGCCCGCACAAAGCGGTGAGCATGTGTTTAAATTCGATGCAAGCGG 1023
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Qy 956 AAAAACCCTTACCTTACCTTGACATGTAGCGAATATTTTAGAGATAAATAGTGCCTCGG 1015
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1024 AAGAACCTTACCAGGGCTTGACATGCCCGCAATCCTCTTGAAGAGAGGGGTGCCCTCGG 1083
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1016 GAACGCTAAACACAGGTGCTGCATGGCTGTCTGAGCTCGTGTCTGAGATGTGCGGTTAA 1075
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1084 GAACGCGGACACAGGTGCTGCATGGCTGTCTGAGCTCGTGCCTGTAAGGTGTGCGTTAA 1143
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1076 GTCCGCAACGAGCGCAACCCCTTGTCTAATATTCGCATCATTTAGTTGGGCACTTTAATG 1135
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1144 GTCTCGCAACGAGCGCAACCCCTGCTGTGTAGTTGCCA-CTATGAGTTTGGAAACCTGAAC 1202
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1136 AGACTGCGCGGTGACAAACCGGAGGAAGTGGGATGAGCTCAAGTCCCTCATGGCCCTTAT 1195
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1203 AGACCGCGCGTGTAAAGCGGAGGAGAGGATGAGGCCAAGTCATCATGCCCTTAT 1262
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1196 GGGTAGGGCTTACACGTAATACATCGCGCTACAGAGGTTGCCAAACCGCGAGGGGG 1255
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1263 GCCCTGGCGGACACACGCTGTACATGGCGGGACAAAGGTCGCGATCTCGCGAGGGTG 1322
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1256 AGCTAATCTCAGAAAGCGGCTGTAGTCCGGATCGGAGTCTGCAACTCGACTCCGTTGAG 1315
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1323 AGCTAACTCCAAAACCCGCTCTCAGTTTCGAGTTGCGAGGCTGCAACTCGCCTGCATGAAG 1382
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1316 TCGGAATCGGTAGTAATCGCGGATCAG-CATGTCGCGTGAATACGTTCCCGGGTCTTGT 1374
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1383 CAGGAATCGGTAGTAATCGCGGTCAGCCATACGCGGCTGTAATCCGTTCCCGGGCTTGT 1442
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1375 ACACACCGCGCTCACACCATGGAGTGGGTTTCCACCAAGAGCAGATAGTC-TAACCGTA 1433
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1443 ACACACCGCGCTCACACTATAGGAGTGGCCATGTTTGAAGTCATTAACCTTAACCGTA 1502
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1434 AGAGGCGTTTGCC 1447
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1503 AGGAGGGGATGCC 1516

RESULT 3
CK296497 941 bp mRNA linear EST 02-AUG-2004
LOCUS EST759211 Nicotiana benthamiana mixed tissue cDNA library,
DEFINITION normalized, full-length Nicotiana benthamiana cDNA clone NBMD226 5'
end, mRNA sequence.
ACCESSION CK296497 GI:39881943
VERSION CK296497.1
KEYWORDS EST.
SOURCE Nicotiana benthamiana
ORGANISM Nicotiana benthamiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
REFERENCE 1 (bases 1 to 941)
AUTHORS Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A., Day,B.,
Staskawicz,B., Jin,H. and Baker,B.
TITLE Generation of EST sequences from Nicotiana benthamiana
JOURNAL Unpublished (2003)
COMMENT Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seq primer: ATT TAG GTG ACA CTA TAG.
FEATURES
1..941
source
1. .941
/organism="Nicotiana benthamiana"
/mol_type="mRNA"
/db_xref="taxon:4100"
/clone="NBMD226"
/tissue_type="abiotic and biotic stress-treated leaves,
callus tissue and root tissue"
/lab_host="DH10B-Tona"
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/clone_lib="Nicotiana benthamiana mixed tissue cDNA
library, normalized, full-length"
/notes="vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid culture
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (Pseudomonas syringae pv tomato 12 hr;
Xanthomonas campestris pv campestris 12 hr, 18hr;
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
amounts."
```

ORIGIN

Query Match 44.3%; Score 650.4; DB 7; Length 941;
Best Local Similarity 82.1%; Pred. No. 2.6e-189;
Matches 772; Conservative 0; Mismatches 166; Indels 2; Gaps 2;

QY 1 TTGATCATGGCTCAGATTGAACGCTGCGCGATGCTTTACACATGCAAGTCGAACGGCAG 60
DB 3 TTGATCATGGCTCAGATTGAACGCTGCGCGAGGCTTAACACATGCAAGTCGAACGGCAG 62

QY 61 CACGGTGTCTGCACCTGGTGGAGTGGCGGCGGTGAGTATGATCGACGACGTC 120
DB 63 CACGGGTACTTGTACCTGGTGGCGGCGGCGGTGAGTATGATCGACGACGTC 122

QY 121 CAGAAATGGGGGATAACGCATCGAAAGATGTCTAATACCGCATATTTCTCTACGGAGGAA 180
DB 123 TGGTAGTGGGGGATAACGCTCGGNAACGGACGCTAATACCGCATACGCTCTACGGAGAA 182

QY 181 AGCAGGGGATCGAAAGACCTTGTCTTTTGGAGCGCGCGATGCTGATAGTAGTTGGT 240
DB 183 AGCAGGGGACCTTGGCGCTTGGCTATCAGATGAGCCTAGGTCGATAGTAGTTGGT 242

QY 241 GGGTAAGCGCTACCAAGCGACGATCAGTAGTTGGTCTGAGAGGACGACCGACAC 300
DB 243 GAGGTAATGGCTACCAAGCGGAGTCCGTAACCTGCTCTGAGAGGATGATCAGTACAC 302

QY 301 TGGGACTGAGACACGGCCCGACACTCTTACGGAGGACGACGTGGGAAATTTGGACAATG 360
DB 303 TGGAACTGAGACACGGTCCAGACTCTTACGGAGGACGACGTGGGAAATTTGGACAATG 362

QY 361 GCGAAAGCCTGATCCAGCAATGCGCGGTGAGTGAAGAAGG-CTTCGGTGTGAAGCTC 419
DB 363 GCGAAAGCCTGATCCAGCAATGCGCGGTGAGTGAAGAAGGCTCTTCGGATTTGAAGCAC 422

QY 420 TTTTCAGTCGAGAAAGAAAGGTTGTGACTAATAATCAACAATGATGTTACCGACAGAA 479
DB 423 TTTTAAGTTGGAGGAGGAGGAGGTTACTCTAATACTGATGTTGTTTACGTTACCGACAGAA 482

QY 480 GAAGCACCGGCTAACTACTGTCACGACGCGCGGTAAATACGTAGGTTGCAAGCGTTAATC 539
DB 483 TAAGCACCGGCTAACTCTGTGCCAGCAGCGCGGTAAATACAGAGGTTGCAAGCGTTAATC 542

QY 540 GGAATTAATGCGGCTAAAGGTCGCGAGGCGGCTTTGTAAGTCAGATGTGAATCCCCGG 599
DB 543 GGAATTAATGCGGCTAAAGGTCGCGAGGCGGCTTTGTAAGTTGAATGTGAATCCCCGG 602

QY 600 GCTTAACTGGGAAATTCGTTTGAACCTTACAAGCTAGAGTGTAGCAGAGGGGGTGGAA 659
DB 603 GCTCAACTGGGAACTGCATCCAAACTGGCAAGCTAGATGTAGAGGGTGTGGAA 662

QY 660 TTCCATGTGTAGCAGTGAATGCGTAGAGATATGGAAGAAATCATCGATGGCGAAGCGACC 719
DB 663 TTTCTGTGTAGCGGTGAATGCGTAGATATAGGAAGAACACCACTGGCGAAGCGACC 722

QY 720 CCCTGGGTAACTGACGCTCAATGCAAGAGGCTGGGAGGCAAAAGGATTAGATACC 779
DB 723 ACCTGGGACTGATCTGACACTGAGGTCGAAAGGCTGGGAGGCAAAAGGATTAGATACC 782

QY 780 CTGGTAGTCACAGCGCTTAACAGATGTCAACTAGTTGTTGGGCGCTTACTAGGCTTGGTAAC 839

783 CTGGTAGTCACGCCCTAAACGATGTCAACTAGCCGTTGGG-AGCCTTGAGCTCTTAGTG 841

QY 840 GTAGCTAACCGCTGAAGTTGACCGCTCGGGAGTACGGTCGCAAGGATTAATACTCAAGG 899

DB 842 GCAGCTAACGCATTAAGTTGACCGCTCGGGAGTACGGCCGCGGCTTAATACTCAATG 901

QY 900 AATTGACGGGAGCCCGCACACAGCGGTGGATTATGTGATT 939

DB 902 AATTGACGGGAGCCCGCACACAGCGGTGGAGCATGTGTTT 941

RESULT 4

BZ439740 1084 bp DNA linear GSS 13-DEC-2002

LOCUS BONDUS4TF BO.1.6.2 KB tot Brassica oleracea genomic clone BONDUS4,

DEFINITION genomic survey sequence.

ACCESSION BZ439740

VERSION BZ439740.1 GI:26695676

KEYWORDS GSS.

SOURCE Brassica oleracea

ORGANISM Brassica oleracea

REFERENCE 1 (bases 1 to 1084)

AUTHORS Ayele,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S., Utterback,T.R., Wortman,J.R., White,O.R. and Town,C.D.

TITLE Whole genome shotgun sequencing of Brassica oleracea and its

JOURNAL application to gene discovery and annotation in Arabidopsis

PUBMED Genome Res. 15 (4), 487-495 (2005)

COMMENT 15805490

Other_GSSs: BONDUS4TR

Contact: Chris Town

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA.

Tel: 301-838-3523

Fax: 301-838-0208

Email: cdtown@tigr.org

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TP

Class: sheared ends.

Location/Qualifiers

1. .1084

/organism="Brassica oleracea"

/mol_type="genomic DNA"

/strain="TO1000DH3"

/db_xref="taxon:3712"

/clone_lib="BO.1.6.2 KB tot"

/notes="Vector: pHO51; Site 1: BstXI; 1.6-2 kb sheared

total DNA inserted into pHO51 using BstXI linkers"

FEATURES

source

ORIGIN

Query Match 43.3%; Score 635; DB 9; Length 1084;
Best Local Similarity 76.9%; Pred. No. 1.6e-184;
Matches 837; Conservative 0; Mismatches 225; Indels 27; Gaps 4;

QY 252 CTACCAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACGACACTGGGACTGAGA 311

DB 3 CTTACCAGGCGATGATCAGTAGCTGGTCCGAGAGGA-GATCAGCCACACTGGGACTGAGA 61

QY 312 CACGCGCCGACGCTCTACGCGAGGACGAGCTGGGGAATTTGGACAATGGCGAAAGCCT 371

DB 62 CACGCGCCGACGCTCTTACGCGAGGACGAGCTGGGGAATTTCCGCAATGGCGAAAGCCT 121

QY 372 GATCCAGCAATGCGCGTGAAGTGAAGAAGG-CTTCGGGTTGTAAAGCTCTTTCACTGTCGAG 430

DB 122 GACGGAGCAATGCGCGTGGAGGTAGAGGCTACGAGCTCTCTGAACTCTTTTCCCAAG 181

QY 431 AAGAAAGGTTGTGACTAATAATCAACAATTATGATGGTACCGCAGAAAGCAGCAGCCGC 490

DB 182 AAG-----AAGCAATGACGCGTATCTGGGGAATAGCATCGGC 218


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Qy 491 TAACTACCTGCGCAGCAGCGCGGTAACTAGTAGGTGCAAGCTTAATCGGAATTAAGTGG 550
Db 219 TAACTCTGTGCGCAGCAGCGCGGTAACTAGTAGGTGCAAGCTTAATCGGAATTAAGTGG 278
Qy 551 GCGTAAAGGGTGGCAGCGCGCTTTGTAGTCAGATGTGAATATCCCGGGCTTAACCTGG 610
Db 279 GCGTAAAGGGTGGCAGCGCGCTTTGTAGTCAGATGTGAATATCCCGGGCTTAACCTGG 338
Qy 611 GAATTCGCTTTCAACTCAAGCTAGATGTAGCAGAGGGGGGTGGAATTCATGTTGA 670
Db 339 GACAGCGGTGGAACTAACAGCTTTAGTACGCTAGCGTAGGGGAGAGGGAATTTCCGGTGA 398
Qy 671 GCAGTGAATCGTAGAGATATGGAAGCACTGATGCGAAGGAGCGCCCTGGGTTAA 730
Db 399 GCGTGAATCGTAGAGATATGGAAGCACTGATGCGAAGGAGCGCCCTGGGTTAA 458
Qy 731 CACTGACCTCATGCAAGAGCGGTGGGAGCAAAACAGATTTAGATACCTCTGGTAGTCCA 790
Db 459 CACTGACCTCATGCAAGAGCGGTGGGAGCAAAACAGATTTAGATACCTCTGGTAGTCCA 518
Qy 791 CGCCTTAACGATGCAACTAGTGTGTTGGGCTTACTAGGCTTG--GTAACTGACTTAAC 848
Db 519 AGCGGTAAACGATGCAACTAGTGTGTTGGGCTTACTAGGCTTG--GTAACTGACTTAAC 578
Qy 849 CGGTGAAGTTCACCGCTGGGAGTACGCTGCGAGATTTAAACTCAAGGAATTTGACGG 908
Db 579 GCGTTAGTATCCCGCTGGGAGTACGCTTGCAGAGATGAATCTCAAGGAATTTGACGG 638
Qy 909 GGACCCGCAAGCGGTGGATTTATGTGATTAATTCGATCAACGCGCAAAACCTTACCT 968
Db 639 GGGCCGCGCAAGCGGTGGATTTATGTGATTAATTCGATCAACGCGCAAAACCTTACCA 698
Qy 969 ACCCTTGACATGATAGCAATATTTAGAGATAAATAGTGCCTTCGGGAAGCTTAACACA 1028
Db 699 GGGCTTGACATGCGCGAATCTCTTGAAGAGAGGGGTGCTTCGGGAAGCTTAACACA 758
Qy 1029 GGTGCTGATGCTGTGCTGAGCTGCTGAGATGTTGGGTTAAGTTCGCGCAACGAG 1088
Db 759 GGTGCTGATGCTGTGCTGAGCTGCTGAGATGTTGGGTTAAGTTCGCGCAACGAG 818
Qy 1089 CGCAACCTTGTCTAATATTCGCATCATTTAGTTGGGCATTTTAAATGAGACTGCGGTGA 1148
Db 819 CGCAACCTTGTCTAATATTCGCATCATTTAGTTGGGCATTTTAAATGAGACTGCGGTGA 878
Qy 1149 CAACCGGAGAGGTGGGATGAGCTCAAGTCTCATGCGCTTATGGTAGGGCTTCA 1208
Db 879 TAAGCGGAGAGGTGGGATGAGCTCAAGTCTCATGCGCTTATGGTAGGGCTTCA 938
Qy 1209 CACGTAAATACATGCGCGTACAGAGGTTGCCAACCGCGAGGGGAGCTAATCTCAGA 1268
Db 939 CACGTAAATACATGCGCGTACAGAGGTTGCCAACCGCGAGGGGAGCTAATCTCAGA 998
Qy 1269 AAGCGCGTGTAGTCGGATCGGAGTCTGCAACTCGACTCGCTGAAGTTCGGAATCGCTAG 1328
Db 999 AAGCGCGTGTAGTCGGATCGGAGTCTGCAACTCGACTCGCTGAAGTTCGGAATCGCTAG 1058
Qy 1329 TAATCGCG 1337
Db 1059 TAATCGCG 1067

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RESULT 5
BH814966/c 1143 bp DNA linear GSS 31-MAY-2003
LOCUS BH814966
DEFINITION pBPC15 Maize B chromosome PCR DNA library Zea mays genomic clone
ACCESSION BH814966
VERSION BH814966.1 GI:31249923
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

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clade: Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 1143)
Cheng,Y.M. and Lin,B.Y.
Cloning and characterization of maize B chromosome sequences
derived from microdissection
Genetics 164 (1), 299-310 (2003)
12750341
Contact: Bor-yaw Lin
Department of Molecular Biology
National Chung Hsing University
250 Kuo Kuang Rd, Taichung 402, Taiwan (ROC)
Tel: 886-4-2285-1885
Fax: 886-4-2287-4879
Email: bylin@dragon.nchu.edu.tw
Insert Length: 1143 Std Error: 0.00
Class: PCR fragment.
Location/Qualifiers
1. 1143
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="L289"
/db_xref="taxon:4577"
/clone="pBPC15"
/sex="hermaphrodite"
/cell_type="Pollen mother cells"
/dev_stage="Meiosis I"
/lab_host="DHSalpa"
/clone_lib="Maize B chromosome PCR DNA library"
/note="Vector: pBSK-; The library was constructed from
microdissected B chromosome DNA."

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ORIGIN
Query Match 43.0%; Score 631.2; DB 9; Length 1143;
Best Local Similarity 89.3%; Pred. No. 2.4e-183;
Matches 738; Conservative 0; Mismatches 78; Indels 10; Gaps 5;

Qy 645 CAGAGGGGGTGGGAATTCATGTGTAGCAGTGAATGCGTAGAGATATGGAAGAACATCG 704
Db 1143 CAGAGGGGGTGGGAATTCATGTGTAGCAGTGAATGCGTAGAGATATGGAAGAACATCG 1084
Qy 705 ATGCGAAGGAGCGCCCTGGTTAACTGACGCTCATGCAAGAACGCTGGGAGCAA 764
Db 1083 ATGCGAAGGAGCGCCCTGGTTAACTGACGCTCATGCAAGAACGCTGGGAGCAA 1024
Qy 765 ACAGATTTAGATACCTGTGTAGTCCAGCCCTTAACGATGTCAACTAGTTGTTGGGCTT 824
Db 1023 ACAGATTTAGATACCTGTGTAGTCCAGCCCTTAACGATGTCTACTAGTTGTTGGGCTT 964
Qy 825 ACTAGGCTTTGTTAAGTGTAACTGAGTAACTGAGTAACTGAGTAACTGAGTAACTGAGT 884
Db 963 AATTGAGCTTTGTTAAGTGTAACTGAGTAACTGAGTAACTGAGTAACTGAGTAACTGAGT 904
Qy 885 ATTTAAACTCAAAGGAATTTGAGCGGGACCCGCAACGCGGTGGATTTATGTGATTAATTC 944
Db 903 ATTTAAACTCAAAGGAATTTGAGCGGGACCCGCAACGCGGTGGATTTATGTGATTAATTC 844
Qy 945 GATGCAACGCGAAGAACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTAC 1004
Db 843 GATGCAACGCGAAGAACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTAC 784
Qy 1005 AGTG--CCTTCGGGAAGCTAAACACAGGTGTGATGCTGTGCTGCTGCTGCTGCTGCTGCTG 1062
Db 783 AGTGCTGGAAGAGAACAGTACACAGGTGTGATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 724
Qy 1063 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1122
Db 723 GATGCTT--GGTTAAGTTCGCGCAACGCGGTGGATTTATGTGATTAATTCGATTAATTCG 670
Qy 1123 GGGCACTTTAATGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1182
Db 669 GGGCACTTCTATGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 611
Qy 1183 TCATGGGCTTTATGGTAGGGCTTTCACAGTAAATACATGCGGTACAGAGGGTTGCCA 1242

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Db610TCATGGCCCTTATGGGTAGGGCTTTCACAGCTCATCAATGGTATCATACAGAGCGCCGCCA551

Qy1243ACCGCGAGGGGAGCTAAATCTCAGAAAGCGCTCGTAGTCCGGATCGGAGTCTGCNACT1302

Db550ACCGCGAGGGGAGCTAAATCGCAGAAAGTGATCGTAGTCCGGATGTAGTCTGCNACT491

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Qy1423GTCTAACCGTAA--GAGGGCGTTTGCCACGCGAGATTCATGACTGG1467

Db370GCTTAAACGAGGAGGGCGCTTACCACGCTAGGATTCGTGACTGG325

RESULT 6

BZ447500/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

BZ447500

BONKF40TR BO 1.6_2_KB tot Brassica oleracea genomic clone BONKF40,

Genomic survey sequence.

BZ447500

BZ447500.1

GI:26712943

Brassica oleracea

Brassica oleracea

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

1

(bases 1 to 1053)

Ayele M., Haas B.J., Kumar N., Wu H., Xiao Y., Van Aken S.,

Uterback T.R., Wortman J.R., White O.R. and Town C.D.

Whole genome shotgun sequencing of Brassica oleracea and its

application to gene discovery and annotation in Arabidopsis

Genome Res. 15 (4), 487-495 (2005)

15805490

Other GSSs: BONKF40TF

Contact: Chris Town

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA.

Tel: 301-838-3523

Fax: 301-838-0208

Email: cdtown@tigr.org

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TR

Class: sheared ends.

FEATURES

source

1..1053

/organism="Brassica oleracea"

/mol_type="genomic DNA"

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/db_xref="taxon:3712"

/clone="BONKF40"

/clone_libs="BO 1.6_2_KB_tot"

/note="Vector: pHOS1; Site 1: BstXI; 1.6-2 kb sheared

total DNA inserted into pHOS1 using BstXI linkers"

ORIGIN

Query Match

Best Local Similarity

Matches

826;

Conservative

0;

Mismatches

223;

Indels

27;

Gaps

4;

Qy215

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274

Db1052

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Qy275

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334

Db992

TGGTCCGAGAGGATGATCAGCCACACTGGGACTGAGACACGGCCCACTCTCAGGGAG

933

Qy335

GCAGCAGTGGGGAATTTTGGACAATGGGGCAAGCCTGATCCAGCAATGCCGCGTGAGTG

394

Db932

GCAGCAGTGGGGAATTTTCG--CAATGGGGCAAGCCTGACGGAGCAATCCCGCGTGAGG

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453

Db873

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Qy454

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513

Db833

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777

Qy514

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717

Qy574

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Db716

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Qy754

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Qy872

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931

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Qy992

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1231

Db116

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57

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1287

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1

RESULT 7

BZ431523/c

LOCUS

DEFINITION

ACCSSION

VERSION

BZ431523

BONHD88TF BO 1.6_2_KB tot Brassica oleracea genomic clone BONHD88,

genomic survey sequence.

BZ431523

BZ431523.1

GI:26677909

1010 bp

DNA

linear

GSS 13-DEC-2002

KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
AUTHORS 1 (bases 1 to 1010)
 Ayele, M., Haas, B.J., Kumar, N., Wu, H., Xiao, Y., Van Aken, S., Uterback, T.R., Wortman, J.R., White, O.R. and Town, C.D.
TITLE Whole genome shotgun sequencing of Brassica oleracea and its application to gene discovery and annotation in Arabidopsis
JOURNAL Genome Res. 15 (4), 487-495 (2005)
PUBMED 15805490
COMMENT Other GSSs: BONHD88TR
 Contact: Chris Town
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdtown@tigr.org
 DNA is from a doubled haploid provided by Tom Osborn.
 Seq primer: TP
 Class: sheared ends.
FEATURES Location/Qualifiers
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 /mol_type="genomic DNA"
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 /clone="BONHD88"
 /clone_lib="BO 1.6-2 KB tot"
 /note="Vector: pROSI; Site 1: BstXI; 1.6-2 kb sheared total DNA inserted into pROSI using BstXI linkers"
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 Best Local Similarity 77.5%; Pred. No. 2.5e-180;
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 1010 GATTAGCTAGTGTGGGTAAGGCTTACCAAGCGCATGATCAGTAGTGTGTGAGAG 951
 286 GACACACGACACATGGGACTGAGACACGGCCAGACTCTACGGGAGGAGCAGCAGTGG 345
 950 GATGATCAGCCACATGGGACTGAGACACGGCCAGACTCTCTACGGGAGGAGCAGTGG 891
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 890 GAATTTTCCGNAATGGGCGAAGGCTGACGGAGCANTGCCGCTGGAGTGAAGGCTTA 831
 405 CGGTTCTGAAGCTCTTTTCAGTCGAGAGAAAGGTTGTGACTAATAATCAAACTTATG 464
 830 CGGTTCTGAAGCTCTTTTCCAGAGAG-----AAGCAATG 794
 465 ATGTACCGACAGAAGACACCGCTTAACTACGTGCAGAGCCGCGGTAAATACGTAGG 524
 793 ACGGTATCTGGGAATAAGCATCGGCTAACTCTGTGCCAGAGCCGCGGTAAATACAGAG 734
 525 GTGCAAGCGTTAATCGGAATTAATCTGGGCTTAAAGGTTGCGAGCGGCTTGTAAAGTCAG 584
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 705 ATGCGGAAGGAGCGCCCTGGGTTAACTCAGCTCATGCCCTCATGCCAAGCGTGGGAGCAA 764

553 ACGGCGAAAGCACTCTCTGCTGGGCGGACACTGACACTGAGAGACGAAGCTAGGCGAGCGA 494
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 433 TCGACCGCTGCACTGCTGTAGCTAACCGTTAGTATCCCGCTGGGGAGTACGTTGCA 374
 883 GGAATTAACCTCAAAAGGAATTGACGGGACCCGCAACGCGGTGGAATATGTTGGAATTAAT 942
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 1123 GGGCATTATGAGACTGCGGTGACAAACCGGAGAGAGTGGGATGAGCTCAGTCC 1182
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 1183 TCATGGCCCTTATGGGTAGGCTTTCACACGTAATACAAATGGCGGTACAGAGGGTTGCA 1242
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 1243 ACCCGGAGGGG 1255
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LOCUS BZ463550 BO 1.6-2 KB tot Brassica oleracea genomic clone BONK86,
DEFINITION genomic survey sequence.
ACCESSION BZ463550
VERSION BZ463550.1 GI:26749465
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
REFERENCE 1 (bases 1 to 1044)
AUTHORS Ayele, M., Haas, B.J., Kumar, N., Wu, H., Xiao, Y., Van Aken, S., Uterback, T.R., Wortman, J.R., White, O.R. and Town, C.D.
TITLE Whole genome shotgun sequencing of Brassica oleracea and its application to gene discovery and annotation in Arabidopsis
JOURNAL Genome Res. 15 (4), 487-495 (2005)
PUBMED 15805490
COMMENT Other GSSs: BONK86TR
 Contact: Chris Town
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdtown@tigr.org
 DNA is from a doubled haploid provided by Tom Osborn.
 Seq primer: TP
 Class: sheared ends.
FEATURES Location/Qualifiers
 source 1..1044
 /organism="Brassica oleracea"
 /mol_type="genomic DNA"

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Db	47	CGAAGTCGTTACCTTAACCGCAAGGAGGGGGCGCGAAGGC	7
RESULT 9			
BZ494182/c			
LOCUS	BZ494182	1051 bp	linear
DEFINITION	BONHR54TR BO 1.6.2 KB tot Brassica oleracea genomic clone BONHR54, genomic survey sequence.		
ACCESSION	BZ494182		
VERSION	BZ494182.1	GI:27004681	
KEYWORDS	GSS.		
SOURCE	Brassica oleracea		
ORGANISM	Brassica oleracea		
REFERENCE	1 (bases 1 to 1051)		
AUTHORS	Ayele,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S., Uterback,T.R., Wortman,J.R., White,O.R. and Town,C.D.		
TITLE	Whole genome shotgun sequencing of Brassica oleracea and its application to gene discovery and annotation in Arabidopsis		
JOURNAL	Genome Res. 15 (4), 487-495 (2005)		
PUBMED	15805490		
COMMENT	Other GSSs: BONHR54TF Contact: Chris Town TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA. Tel: 301-838-3523 Fax: 301-838-0208 Email: cdtown@tigr.org DNA is from a doubled haploid provided by Tom Osborn. Seq primer: TR Class: sheared ends.		
FEATURES	Location/Qualifiers 1..1051 /organism="Brassica oleracea" /mol_type="genomic DNA" /strain="TO1000DH3" /db_xref="taxon:3712" /clone="BONHR54" /clone_lib="BO 1.6.2 KB tot" /note="vector: pHO51; Site 1: BstXI; 1.6-2 kb sheared total DNA inserted into pHO51 using BstXI linkers"		
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Matches	774;	Conservative	0; Mismatches 224; Indels 3; Gaps 2;
Qy	455	ACAACTTATGATGGTACCGACAGAGAACGACCGGCTAACTACGTGCGACGACGCGGT	514
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Qy	515	AATACGTAGGTGCNAGCGTTAATCGGAATTACTGGCGGTAAAGGGTGCACGCGCGCTT	574
Db	947	AATACAGAGATGCAAGCGTTATCCGGAATGATTGGCGGTAAAGCGTCTGTAGTGGCTT	888
Qy	575	TGTAAGTCAGATGTGAATCCCGGGCTTAACTGGGAATTGCGTTGAAACTACAAAGC	634
Db	887	TTTAAAGTCGCGCTCAATCCAGGGCTCAACCTCGACAGCGGTGGAACCTACCAAGC	828
Qy	635	TAGAGTGTAGCAGAGGGGGTGGAAATTCATGTGTAGCAGTGAATTCGCTAGAGATATGG	694
Db	827	TTGAGTACGGTAGGGGACAGAGGGAATTTCCGGTGGAGCGGTGAATTCGCTAGAGATCGGA	768
Qy	695	AAGAACATCGATGGCGAAGGACGCCCTCTGGGTTAACTGACGCTCATGTCACGAAAGCG	754
Db	767	AGAACACCAACGCGGNAAGCACTCTGCTGGCGCGACACTGACACTGAGAGACGAAAGCT	708
Qy	755	TGGGAGCAAAACAGATTAGATACCTCTGGTAGTCCAGCCCTAAACGATGTCAACTAGTT	814
Db	707	AGGGAGCGAATGGGATTAGATACCCAGTAGTCTTAGCCGTTAAACGATGATAGGC	648
Qy	815	GTTGGGCTTACTAGGCTTG--GTAACTGACTAACCGGTGAAGTTGACCGCTGGGGAG	872
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Qy	873	TACGGTCCAGGATTAAACCTCAAGGAATTTGACGGGGACCGCACAGCGGTGGATTAT	932
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Qy	993	TAGAGATAAATAGTGCCTTCGGGAACGCTTAACACAGGTGTCATGGCTGTGCTCAGCT	1052
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Qy	1113	TCATTTAGTTGGGCACTTTAATGAGACTGCGCGGTGACAAACCGGAGGAAGTTGGGATGA	1172
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 Db
 347 CCGTTAGTTTGGAAACCTCGAACGACTGCCGCTGATGAAGCCGGAGGAGGTGAGATGA 288
 Qy
 1173 CGTCAAGTCTCATGGCCCTTATGGGTAGGGCTTTCACACGTAATACAAATGGCGGTACAG 1232
 Db
 287 CGTCAAGTCTCATGGCCCTTATGCCCTGGGGGACACACAGGTGTACAAATGGCGGACAA 228
 Qy
 1233 AGGTTGCAACCGCGAGGGGAGCTAATCTCAGAAAGCCGCTGTAGTCCGGATCGGA 1292
 Db
 227 AGGTTGCGGATCCCGCGAGGGTGAGCTAACTCCAAACCCGCTCTCAGTTCCGATTGCA 168
 Qy
 1293 GTCTGCAACTCGACTCCGTAAGTTCGGAATCGCTAGTAATCGCGGATCAG--CAGTCCGG 1351
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 167 GCCTGCAACTCGCTTCGATGAAGCCGGAAATCGCTAGTAATCGCCGCTCAGCAGCGCG 108
 Qy
 1352 GTGAATAGCTTCCGGGCTTTGTACACACCGCCGCTCACACATGGGAGTGGGTTTCACC 1411
 Db
 107 GTGAATTCGTTCCGGGCTTTGTACACACACCGCCGCTCACACTATGGGAGCTGGCCATGCC 48
 Qy
 1412 AGAAGCAGATGCTTAACCGTAAGAGGGCGTTTGCACGGC 1452
 Db
 47 AAAAGTCGTTACCTTAACCGCAAGGAGGGGGGCGCAAGGC 7

RESULT 10
 CK280527
 LOCUS
 DEFINITION
 EST743249 Nicotiana benthamiana mixed tissue cDNA library,
 normalized, full-length Nicotiana benthamiana cDNA clone NEWALL7 5'
 end, mRNA sequence.
 CK280527
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Nicotiana benthamiana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliopsida; eudicotyledons; core eudicotyledons;
 asterids; lamids; Solanales; Solanaceae; Nicotiana.
 Buell, C.R., Hart, A., Ziesmann, V., Karamycheva, S.A., Day, B.,
 Staskiewicz, B., Jin, H. and Baker, B.
 Generation of EST sequences from Nicotiana benthamiana
 Unpublished (2003)
 JOURNAL
 COMMENT
 Other ESTs: EST743250
 Contact: Robin Buell
 The Institute for Genomic Research
 9712 Medical Center Dr, Rockville, MD 20850, USA

Email: potato-array@tigr.org
 Clones can be requested from the University of Arizona Genomics
 Institute via http://genome.arizona.edu/orders/
 Seq primer: ATT TAG GTG ACA CTA TAG.
 Location/Qualifiers
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 callus tissue and root tissue"
 /lab_host="DH10B-Tona"
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 /notes="vector: pCMVSPORT6.1; Site_1: EcoRI; Site_2: NotI;
 supplier: RNA was isolated from Nicotiana benthamiana
 tissues that include callus, roots from liquid culture
 grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
 cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
 challenged leaves (Pseudomonas syringae pv tomato 12 hr;
 Xanthomonas campestris pv campestris 12 hr, 18hr;
 Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
 campestris pv vesicatoria 18hr). RNA was isolated from
 these tissues and pooled in approximately equal molar
 amounts."

ORIGIN

Query Match 41.9%; Score 614; DB 7; Length 889;
 Best Local Similarity 82.3%; Pred. No. 4.7e-178;
 Matches 729; Conservative 0; Mismatches 155; Indels 2; Gaps 2;
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 Db 3 TTGATCATGCTCAGATGTAACGCTGGCGGATCTTTACACATGCAAGTCGACGGCAG 62
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 Db 423 TTTAAGTTGGAGGAGGAGGAGGAGTACCTAATACGTTGATTTGTCAGTTACCCAGCAGNA 482
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 Db 483 TAAGCAGCGGCTAATCTCTGTGCCAGCAGCGCGGTGAATACAGAGGGTGCAGACGTTAATC 542
 Qy 540 GGAATTAATCTGCGGTAAAGGTTGCGAGGCGGCTTGTGTAAGTCAAGTGTGAATCCCCGG 599
 Db 543 GGAATTAATCTGCGGTAAAGGTTGCGAGGCGGCTTGTGTAAGTCAAGTGTGAATCCCCGG 602
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Db

603

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662

Qy

660

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719

Db

663

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722

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720

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779

Db

723

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782

Qy

780

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838

Db

783

|||||

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842

Qy

839

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CGTAGCTAAACGCGTGAATGTGACCGCTGGGGAGTAGCGTCGCAGG

884

Db

843

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888

RESULT 11

BZ426201/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PURVED

COMMENT

1016 bp

DNA

linear

GSS 13-DEC-2002

BONDZ28TF BO_1.6_2_KB_tot

Brassica oleracea

genomic clone

BONDZ28,

genomic survey sequence.

BZ426201

BZ426201.1

GI:26667713

GSS.

Brassica oleracea

Brassica oleracea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 1016)

Ayele,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S., Utterback,I.R., Wortman,J.R., White,O.R. and Town,C.D.

Whole genome shotgun sequencing of Brassica oleracea and its application to gene discovery and annotation in Arabidopsis

Genome Res. 15 (4), 487-495 (2005)

15805490

Other GSSs: BONDZ28TR

Contact: Chris Town

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA.

Tel: 301-838-3523

Fax: 301-838-0208

Email: cdtown@tigr.org

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TF

Class: sheared ends.

Location/Qualifiers

1..1016

/organism="Brassica oleracea"

/mol_type="genomic DNA"

/strain="TO1000DH3"

/db_xref="taxon:3712"

/clone="BONDZ28"

/clone_lib="BO_1.6_2_KB_tot"

/notes="Vector: pHOS1; Site 1: BatX1; 1.6-2 kb sheared total DNA inserted into pHOS1 using BatX1 linkers"

ORIGIN

Query Match

Best Local Similarity

Matches

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77.5%; Pred. No. 5.6e-178;

0; Mismatches 207; Indels 27; Gaps 4;

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215

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274

Db

1015

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956

Qy

275

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334

Db

955

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896

Qy

335

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394

Db

895

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837

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395

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453

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836

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797

Qy

454

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513

Db

796

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740

Qy

514

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573

Db

739

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633

Db

679

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620

Qy

634

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693

Db

619

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Qy

694

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753

Db

559

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500

Qy

754

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813

Db

499

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440

Qy

814

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871

Db

439

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380

Qy

872

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931

Db

379

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320

Qy

932

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991

Db

319

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260

Qy

992

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1051

Db

259

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200

Qy

1052

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1111

Db

199

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140

Qy

1112

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1171

Db

139

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80

Qy

1172

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1231

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79

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1232

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Db

19

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RESULT 12

BH705272

LOCUS

DEFINITION

ACCESSION

VERSION

1079 bp

DNA

linear

GSS 20-FEB-2002

BH705272

BOMKA47TF BO_2_3_KB

Brassica oleracea

genomic clone

BOMKA47,

genomic survey sequence.

BH705272

BH705272.1

GI:18787746

KEYWORDS
SOURCE GSS.
ORGANISM Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
AUTHORS 1 (bases 1 to 1079)
 Ayele, M., Haas, B.J., Kumar, N., Wu, H., Xiao, Y., Van Aken, S.,
 Utterback, T.R., Wortman, J.R., White, O.R. and Town, C.D.
TITLE Whole genome shotgun sequencing of Brassica oleracea and its
 application to gene discovery and annotation in Arabidopsis
JOURNAL Genome Res. 15 (4), 487-495 (2005)
PUBMED 15805490
COMMENT Other GSSs: BOMKA47TR
 Contact: Chris Town
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdtown@tigr.org
 DNA is from a doubled haploid provided by Tom Osborn.
 Seq primer: TF
 Class: sheared ends.
FEATURES
 source
 Location/Qualifiers
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 /mol_type="genomic DNA"
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 genomic DNA inserted into pGOS1 using BatXI linkers"
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 Best Local Similarity 76.3%; Pred. No. 8.7e-178;
 Matches 803; Conservative 0; Mismatches 223; Indels 26; Gaps 3;
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 QY 270 GTAGTTGTCTGAGAGGACGACGACACCTGGGACTGACACAGCGGCCAGACTCTCTAC 329
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 DB 276 -----AAGCAATGACGGTATCTGGGGAATAGCATCGGCTAATCTGTGCCAGCAGC 327
 QY 509 CGCGTATACGTAGGGTGCAGGCTTAAATCGGAATTAATCGGGGTAAAGGGTGGCAGG 568
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 QY 569 CGGCTTTGATGATGATGTAATATCCCGGGCTTAACCTGGGAATTCGGTTGAAACTA 628
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 QY 689 ATATGAAGAATCATGATGGCGAAGGCGAGCCCTGGGTTAACTGACGCTCATGCAACG 748

DB 508 ATCGAAAGAAACACCAACCGCGAAAGCACTCTGCTGGGCCGCACTGACACTGAGAGACG 567
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LOCUS BOMJZ86TF BO 2.3 KB Brassica oleracea genomic clone BOMJZ86,
 genomic survey sequence.
ACCESSION BH656222
VERSION BH656222.1 GI:18714532
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
AUTHORS 1 (bases 1 to 1031)
 Ayele, M., Haas, B.J., Kumar, N., Wu, H., Xiao, Y., Van Aken, S.,
 Utterback, T.R., Wortman, J.R., White, O.R. and Town, C.D.
TITLE Whole genome shotgun sequencing of Brassica oleracea and its
 application to gene discovery and annotation in Arabidopsis
JOURNAL Genome Res. 15 (4), 487-495 (2005)
PUBMED 15805490
COMMENT Contact: Chris Town
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdtown@tigr.org
 DNA is from a doubled haploid provided by Tom Osborn.
 Seq primer: TF
 Class: sheared ends.
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 Location/Qualifiers
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 /organism="Brassica oleracea"
 /mol_type="genomic DNA"
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Best Local Similarity 76.3%; Pred. No. 1.3e-177;
Matches 803; Conservative 0; Mismatches 224; Indels 26; Gaps 3;

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Qy 441 TGTGACTAATAATCACACTTATGATGGTACCGACAGAGAACCCGGCTAAGTCTAGCTG 500
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Qy 801 GATGTCAACTAGTGTGTGGGCGCTTACTAGGCTTG--GTAAGTGTAGTAAACCGTGAAGTT 858
Db 574 GATGGATACTAGGCGCTGTGGGTATCGACCCGTCAGTGTGTAGTAAACCGGTTAAGTA 515
Qy 859 GACGCGCTGGGAGTACGCTCGCAGGATTAAATCTCAAGAGAAATTGACGGGACCCGCAC 918
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DEFINITION genomic survey sequence.
ACCESSION BZ450751
VERSION BZ450751.1 GI:26721334
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 1077)
AUTHORS Ayele M. Haas, B.J., Kumar, N., Wu, H., Xiao, Y., Van Aken, S.,
Utechtack, T.R., Wortman, J.R., White, O.R. and Town, C.D.
TITLE Whole genome shotgun sequencing of Brassica oleracea and its
application to gene discovery and annotation in Arabidopsis
JOURNAL Genome Res. 15 (4), 487-495 (2005)
PUBMED 15805490
COMMENT Other GSSs: BONBQ63TF
Contact: Chris Town
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
source 1..1077
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO100DH3"
/db_xref="taxon:3712"
/clone="BONBQ63"
/clone_lib="BO.1.6.2_KB_tot"
/notes="Vector: pHOS1; site 1: BetXI; 1.6-2 kb sheared
total DNA inserted into pHOS1 using BatXI linkers"

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Best Local Similarity 76.9%; Pred. No. 2.7e-177;
Matches 772; Conservative 0; Mismatches 229; Indels 3; Gaps 2;

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Qy 515 AATACGTAGGCGTCAAGCGTTAATCGGAATTAATCGCGCTAAAGGTTGCCAGCGGCTT 574
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Qy 301 AAGAACACCAACGCGGAAGCACTCTGCTGGCCGACACTGACACTGAGACGGAAGCT 360
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Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 601 TTGAAAGAGAGGGTGCCTTCGGGAACCGGACACAGGTGTCATGGCTGCTGCTAGCT 660
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1053 CGTGTGCGTGAATGTTGGGTTAAGTCCCGCAACGAGCGCAACCTTGTCAATTTGCCA 1112
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 661 CTTGCCGTAAAGTGTGGGTTAAGTCCCGCAACGAGCGCAACCTTGTGGTTAGTTGCCA 720
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1113 TCATTTAGTTGGCACTTTAATAGACTCCCGTGACAAACCGGAGGAAGTGGGATGA 1172
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 721 CCGTTAGTTTGAACCTCGAACAGACTCCCGGTGATTAAGCCGAGGAAGGTGAGGATGA 780
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1173 GTCAGTCTCTGTCAGTGGGCTTATGGTAGGCTTACAGCTTAATACATGCGGTACAG 1232
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 781 CGTCAAGTCATATGCCCTTATGCCCTGGGCGACACACGCTGTACAATGGCCCGGACAA 840
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1233 AGGGTTGCAACCCCGAGGGGAGCTAATCTCAGAAAGCGGCTGCTAGTCGGATCGGA 1292
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 841 AGGGTCGGATCCCGGAGGGTGAGTAACTCCAAAACCCGCTCTCAGTTCCGATTGCA 900
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1293 GTCTGCAACTCGACTCCGTGAAGTCGGAATCGTAGTAATCGCGATCAG-CATGTGCG 1351
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 901 GGCTGCAACTCGCTGTCATGAAGCGGGAATCGTAGTAATCGCGGTGAGCCATACGGCG 960
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1352 GTGAATAGTTCGGGCTTGTATACACACCGCGCTGACACCATGCGGAGTGGTTTACC 1411
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 961 GTGAATTCGTTCCCGGGCTTGTATACACACCGCGCTGACATATGGGAGCTGGCCATGCC 1020
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1412 AGAAGCAGATAGTCTAACCGTAAGAGGGCGTTTGCCACGGCGAG 1455
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Qy 1021 CGAAGTCTTAACTTAAACCGAGGAGGGGTGCGGAGGCGAG 1064
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RESULT 15
CK280528 884 bp mRNA linear EST 02-AUG-2004
LOCUS EST743250 Nicotiana benthamiana mixed tissue cDNA library,
DEFINITION normalized, full-length Nicotiana benthamiana cDNA clone NBMA117 5'
end, mRNA sequence.
ACCESSION CK280528
VERSION CK280528.1 GI:39850200
KEYWORDS EST.
SOURCE Nicotiana benthamiana
ORGANISM Nicotiana benthamiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
REFERENCE 1 (bases 1 to 884)
AUTHORS Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
Staskawicz, B., Jin, H. and Baker, B.
TITLE Generation of EST sequences from Nicotiana benthamiana
JOURNAL Unpublished (2003)
COMMENT Other_ESTs: EST743249
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FEATURES

source 1..884

organism="Nicotiana benthamiana"

mol_type="mRNA"

db_xref="taxon:4100"

clones="NBMA117"

tissue_type="abiotic and biotic stress-treated leaves, callus tissue and root tissue"

lab_hosts="DHI08-Tona"

clone_lib="Nicotiana benthamiana mixed tissue cDNA library, normalized, full-length"

note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI; supplier: RNA was isolated from Nicotiana benthamiana tissues that include callus, roots from liquid culture grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr), cold-stressed leaves (5 C 3 hr, 6hr), and pathogen challenged leaves (Pseudomonas syringae pv tomato 12 hr; Xanthomonas campestris pv campestris 12 hr, 18hr; Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas campestris pv vesicatoria 18hr). RNA was isolated from these tissues and pooled in approximately equal molar amounts."

ORIGIN

Query Match 41.6%; Score 610; DB 7; Length 884;

Best Local Similarity 82.2%; Pred. No. 8.1e-177; Indels 2; Gaps 2;

Matches 725; Conservative 0; Mismatches 155;

Qy 1 TTGATCATGGCTCAGATTGAACGCTGGCGGATCTTTACACATGCAAGTCGAAACGGCAG 60

Db 3 TTCATCATGGCTCAGATTGAACGCTGGCGGATCTTTACACATGCAAGTCGAAACGGCAG 62

Qy 61 CACGGGTCTTTCACCTGGTGGCGAGTGGCGGAGTGAATGATCGAAGCGTGTG 120

Db 63 CACGGGTACTTTGTACCTGGTGGCGAGCGGCGAGTGAATGATCGTGTGATCTGCC 122

Qy 121 CAGAAGTGGGGGATAACGCATCGAAAGATGTGCTAACTACCGCATATCTCTACGAGGAA 180

Db 123 TGGTAGTGGGGGATAACGCATCGAAAGATGTGCTAACTACCGCATATCTCTACGAGGAA 182

Qy 181 AGCAGGGGATCGAAAGACCTTTGTGCTTTTGGAGCGCGGATGCTCTAGTGTAGTGTG 240

Db 183 AGCAGGGGACCTTCGGGCTTTGCGCTATCAGATGAGCTAGTGTGATGTAGTGTG 242

Qy 241 GGGGTAAGGCTTACCAAGGCAACGATGATGTTGTTCTGAGAGGACGACGACGACAC 300

Db 243 GAGGTAATGGCTCACCAAGGCGAGATCCGTAATCGTCTCGAGAGGATGATCAGTCACAC 302

Qy 301 TGGGACTGAGACACGCGCCGACCTCTACGAGGAGCGAGCTGGGGAATTTTGGACAATG 360

Db 303 TGGAACTGAGACACGCGTCCAGCTCTACGAGGAGCGAGCTGGGGAATTTTGGACAATG 362

Qy 361 GCGGAAAGCCTGATCCAGCAATGCGCGGTGAGTGAAGAAGG-CTTGGGTTGTAAAGCTC 419

Db 363 GCGGAAAGCCTGATCCAGCAATGCGCGGTGAGTGAAGAAGGCTTCGGAATGTAAAGCAC 422

Qy 420 TTTGAGTGGAGAGAGAAAGGTTGTGATTAATAATACAACTTATGATGATGATGATGATG 479

Db 423 TTTAAGTTGGAGAGAGAGGAGGAGTGTACCTAATACGTTGTTTGTGACGTTTACCGACAG 482

Qy 480 GAACACCGGTAACACTACGTCGACGAGCGCGGTGATACGTCAGGTCGACGCGTTAATC 539

Db 483 TAAGCACCGGTAACACTCTGTGCGGAGCGCGGTGATACGAGGTCGACGCGTTAATC 542

Qy 540 GGAATTAATCTGGGCGTAAAGGCTGCGAGCGGCTTTGTGTAAGTCAGATGTGAAATCCCCCG 599

Db	543	GGATTACTGGCGTAAAGCGCGGTAGTGGTTTGTAAAGTTGGATGTGAAATCCCGG	602
Qy	600	GCTTAACCTGGGAATTGCGTTTGAAGCTCAAAAGCTAGAGTGTAGCAGAGGGGGTGGAA	659
Db	603	GCTCAACCTGGGAACCTGCATCCAAAACCTGGCAAGCTAGAGTATGGTAGAGGGTGGTGGAA	662
Qy	660	TTCCATGTGTAGCAGTGAATGGTAGAGATATGGAAGAACATCGATGGCGAAAGGCAGCC	719
Db	663	TTTCCTGTGTAGCGGTGAATGGGTAGATATAGGAGGAACACCAAGTGGCGNAGGCGACC	722
Qy	720	CCCTGGGTTAACACTGACGCTCATGCAAGAAAGCGTGGGGAGCAAAACAGGATTAGATACC	779
Db	723	ACCTGGACTGATACTGACACTGAGGTGCGAAAGCGTGGGAGCAAAACAGGATTAGATACC	782
Qy	780	CTGCTAGTCCACGCCCTAAACGATGTCAACTAGTTGTTGGG-CCTTACTAGGCTTGGTAA	838
Db	783	CTGCTAGTCCACGCCCTAAACGATGTCAACTAGCCGTTGGGAGCCTTGAGCTCTTAGTGG	842
Qy	839	CGTAGCTAAACGCGTGAAGTTGACCGCCTGGGGAGTACGTCG	880
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Job time : 6264 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 6, 2006, 19:23:40 ; Search time 295 Seconds
(without alignments)
8839.603 Million cell updates/sec

Title: US-10-659-983A-18

Perfect score: 1467

Sequence: 1 ttgatcatggtcagattga.....acggcgagattcatgactgg 1467

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

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- 2: /cgn2_6/ptodata/1/ina/5 COMB.seq:*
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- 8: /cgn2_6/ptodata/1/ina/RE COMB.seq:*
- 9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1115	76.0	1536	US-08-642-229A-1	Sequence 1, Appli
2	1104	75.3	1536	US-08-114-695A-7	Sequence 7, Appli
3	1092.2	74.5	1474	US-08-114-695A-8	Sequence 8, Appli
4	1090.4	74.3	1544	US-09-726-774-5	Sequence 5, Appli
5	1084.8	73.9	1453	US-09-735-567-4	Sequence 4, Appli
6	1081.6	73.7	1455	US-08-642-229A-3	Sequence 3, Appli
7	1078.2	73.5	1451	US-09-342-579-1	Sequence 1, Appli
8	1078.2	73.5	1451	US-09-617-854A-1	Sequence 1, Appli
9	1066.8	72.7	1452	US-08-642-229A-2	Sequence 2, Appli
10	1054.6	71.9	1495	US-09-063-898-1	Sequence 1, Appli
11	1054.6	71.9	1495	US-09-985-846-1	Sequence 1, Appli
12	1054.6	71.5	1467	US-09-735-567-2	Sequence 2, Appli
13	1048.4	71.5	1539	US-09-735-567-6	Sequence 6, Appli
14	1047.8	71.4	1454	US-09-735-567-7	Sequence 7, Appli
15	1037.6	70.7	1540	US-09-228-184-1	Sequence 1, Appli
16	1037.6	70.7	1540	US-09-967-376-1	Sequence 1, Appli
17	1025.4	69.9	1450	US-09-735-567-3	Sequence 3, Appli
18	1012.6	69.0	1484	US-08-632-470-53	Sequence 53, Appli
19	1012.4	68.0	1481	US-09-737-297-4	Sequence 4, Appli
20	1008.2	68.7	1501	US-09-793-920A-1	Sequence 1, Appli
21	1008.2	68.7	1501	US-09-821-016-5	Sequence 5, Appli
22	1008.2	68.7	1501	US-09-745-476-1	Sequence 1, Appli
23	1008.2	68.7	1501	US-09-748-205-1	Sequence 1, Appli
24	1008.2	68.7	1501	US-09-951-720-1	Sequence 1, Appli

25	1008.2	68.7	1501	3	US-10-411-319-1	Sequence 1, Appli
26	1008.2	68.7	1501	3	US-10-105-305-1	Sequence 1, Appli
27	1008.2	68.7	1501	3	US-10-266-787-5	Sequence 5, Appli
28	1008.2	68.7	1501	3	US-09-791-610-1	Sequence 1, Appli
29	1008.2	68.7	1501	3	US-10-252-518-5	Sequence 5, Appli
30	1001.6	68.3	1518	2	US-08-114-695A-6	Sequence 6, Appli
31	997.8	68.0	1449	3	US-09-602-417-1	Sequence 1, Appli
32	992.2	67.6	1486	3	US-09-737-297-1	Sequence 1, Appli
33	989.4	67.4	26223	3	US-09-596-002-41	Sequence 41, Appli
34	986.2	67.2	1424	3	US-10-007-527A-12	Sequence 12, Appli
35	982.8	67.0	1467	3	US-09-726-774-3	Sequence 3, Appli
36	981.2	66.9	1541	3	US-09-726-774-2	Sequence 2, Appli
37	979.2	66.7	1830121	3	US-09-557-884-1	Sequence 1, Appli
38	979.2	66.7	1830121	3	US-09-557-884-1	Sequence 1, Appli
39	979.2	66.7	1830121	3	US-09-643-990A-1	Sequence 1, Appli
40	979.2	66.7	1830121	3	US-09-643-990A-1	Sequence 1, Appli
41	979.2	66.7	1830121	3	US-10-158-865-1	Sequence 1, Appli
42	979.2	66.7	1830121	3	US-10-158-865-1	Sequence 1, Appli
43	978.2	66.7	1542	2	US-08-757-653-158	Sequence 158, App
44	978.2	66.7	1542	3	US-09-465-355-2	Sequence 2, Appli
45	978.2	66.7	1542	3	US-08-520-946-158	Sequence 158, App

ALIGNMENTS

RESULT 1
US-08-642-229A-1
; Sequence 1, Application US/08642229A
; Patent No. 5874291
; GENERAL INFORMATION:
; APPLICANT: Herwig, Russell P.
; APPLICANT: Bielefeldt, Angela R.
; APPLICANT: Strand, Stuart E.
; APPLICANT: Strand, Stuart E.
; TITLE OF INVENTION: Degradation of Environmental Toxins by a
; TITLE OF INVENTION: Filamentous Bacterium
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christensen O'Connor Johnson and Kindness PLLC
; STREET: 1420 Fifth Avenue, Suite 2800
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: WA 98101-2347
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/642,229A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/246,865
; FILING DATE: 20-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sheiness, Diana K.
; REGISTRATION NUMBER: 35,356
; REFERENCE/DOCKET NUMBER: UOFW19233
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 682 8100
; TELEFAX: (206) 224 0779
; TELEX: 4938023
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1536 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: nucleic acid
; DESCRIPTION: "16S ribosomal DNA"

;
 ; HYPOTHETICAL: NO
 ;
 ; ANTI-SENSE: NO
 ;
 ; ORIGINAL SOURCE:
 ; ORGANISM: *Comamonas testosteroni* ATCC No. 5874291 11996
 US-08-642-229A-1

Query Match 76.0%; Score 1115; DB 2; Length 1536;
Best Local Similarity 87.2%; Pred. No. 0;
Matches 1282: Conservative 0; Mismatches 180; Indels 9

Qy	1	TTGATCATGGCTCAGATTGAACGCTGGCGCATGCTTTACACATGCACAGTGCACGACGGAG	60
Db	14	TTGATCTTGGCTCGAGATTGAACGCTGGCGGCAATGCTTTACATGCACATGTCGAAACGGTAA	73
Qy	61	CACGGGTGCTTGCACTCGTGGCGAGTGGCGGACGGGTGAGTAATGCATCGGAAAGTGTGC	120
Db	74	CA----GGTCTTCGATGCTGACGAGTGGCGNACGGGTGAGTAATACATCGNAACGTGCC	129
Qy	121	CAGAAAGTGGGGATAAACGATCGAAAGATGTGCTAATACCGCANATTTCTCTACGAGGAA	180
Db	130	TAGTAGTGGGGATAACTACTCGAAAGAGTAGCTAATACCGCATGAGATCTACGGATGAA	189
Qy	181	ACAGGGGATCGAAGACCTTGTGCTTTGGAGGGCGGATGCTCATTTAGCTAGTCTAGTGGT	240
Db	190	AGCAGGGGACCTTTCGGGCTTTGTGCTACTAGCGGCTGATGCGCATTTAGGTAGTGGT	249
Qy	241	GGGGTAAGGCTCTCAAGGCAACGATCAGTAGTGTGCTGAGAGACGACACGACCAACAC	300
Db	250	GGGGTAAGGCTTCAAGGCTTGGATCTGTAGCTGTCTGAGAGAGCGACGACGACGACAC	309
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Qy	361	GGCGAAAGCTGATCCAGCAATGCCGGTGTAGTGAAGAGG-CTTGGGTTGTGAAGCTC	419
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TELEFAX: 612-339-3061
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1474 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: rRNA
; ORGANISM: Pseudomonas cepacia
; US-08-114-695A-8

Query Match 74.5%; Score 1092.2; DB 2; Length 1474;
Best Local Similarity 68.3%; Pred. No. 0;
Matches 996; Conservative 252; Mismatches 202; Indels 9; Gaps 4;

QY 1 TTGATCATGGCTCAGATTGAACGCTGGCGGATGCTTTACATGCAAGTCGAACGGC-A 59
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QY 60 GCACGGGTGCTTGACCTGTGGCGAGTGGCGGACGGTGAAGTAATGCATCGGAACGTGT 119
DB 73 GCAUCGGGUGUUNACCUUGGCGAGUGGCGCAACGGGUGAGUAAUACAUGGGAACAU 132
QY 120 CCAGAAAGTGGGGATTAACGCATCGAAAGATGTGCTAATACCGCATATCTCTACGGAGGA 179
DB 133 CCUGUAGUGGGGUAUAGCNCGGCGAAGCCNNAUUAUACCGCAUACGAUACGGAUGA 192
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DB 193 AAGCGGNGACCUUGGGCCUUGCGCUAAGGUGGCGGAGGUGGCGAUGAUAGUUGUUG 252
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DB 253 UGGGUAAGGCUUACCAAGGCGGAGCAUACUAGCUNGUCUGAGAGGAGCAGCAGCCACA 312
QY 300 CTGGGACTTGAGACACGGCCACAGATCTCTA CCGGAGGAGCAGAGTGGGNAATTTCGACAT 359
DB 313 CUGGACUGAGACACGGCCCGACGACUCCUACCGGAGGCGACGAGUGGGGAAUUUUGGACA 372
QY 360 GGGCGAAGGCTGATCCAGCAATGCGGTCGAGTGAAGAGG-CTTCGGGTGTTAAAGCT 418
DB 373 GGGCGAAGGCTGATCCAGCAATGCGGTCGAGTGAAGAGG-CTTCGGGTGTTAAAGCT 432
QY 419 CTTTCAGTCGAGAGAAAGGTTGTGACTAATAATCAAACTTATGATGTTACCGACAGA 478
DB 433 CUUUUGCCGGAGAAAUUCCUUGGCUUAAUACAGCGCGGGGAGUACGAGUACCGGAAGA 492
QY 479 AGAAGACCGGCTAAGTCCAGCAGCAGCGCGGTATATAGTAGGGTGCAAGGCTTAAT 538
DB 493 AUAAGCACCGGCUAACUGGUCNAGCAGCGCGGNNNAUACGUAAGGUGGCAAGCGUUAAU 552
QY 539 CGGAATTACTGGGCTTAAAGGGTGGCGAGCGGCTTTGTAAGTCAAGTGTGAATCCCGG 598
DB 553 CGGAUUUACUGGGCUUAAAGCGUGCGCAGCGGUGUUGUACGAGCCGUAUGAUAUCCCG 612
QY 599 GGGTTAACTGGGAAATGCGTTTGAACCTAACAGCTAGATGTAGCAGAGGGGGTGA 658
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QY 839 CGTAGCTAACGCGTGAAGTTGACCGCTGGGGAGTAGCGGTTCGCGAGGATTTAAACTCAAAG 898
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US-09-726-774-5
; Sequence 5, Application US/09726774
; Patent No. 6677153
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick L.
; TITLE OF INVENTION: Antisense Antibacterial Method and
; TITLE OF INVENTION: Composition
; FILE REFERENCE: 0450-0032.30
; CURRENT APPLICATION NUMBER: US/09/726,774
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 60/168,150
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1544
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoea
US-09-726-774-5
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Query Match 74.3%; Score 1090.4; DB 3; Length 1544;
Best Local Similarity 85.5%; Pred. No. 0;
Matches 1261; Conservative 0; Mismatches 206; Indels 7; Gaps 4;

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DB 14 TTGATCCTGGCTCAGATTGAACGCTGGCGGATGCTTTACATGCAAGTCGGAGCGGCG 73
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Qy 61 CACGGGTCTTGCAC-----CTGGTGGCGAGTGGCGGACGGGTGAGTAATGATCATCGGAACG 116
Db 74 CACAGGGAAGCTTCTCGGTGGCGAGTGGCGAAGCGGTGAGTAACATATCGGAACG 133
Qy 117 TGTCCAGAAGTGGGGATAACCGCATCGAAGATGTCTTAATAACCGCATATTTCTTACCGGA 176
Db 134 TACCGGGTAGCGGGGGATAACTGATCGAAGATCAGCTTAATACCGCATACGCTCTTGAGAG 193
Qy 177 GGAAGACAGGGGATCGAAGACCTTGTCTTTTGGAGCGGCGCGATGCTGTATGATAGCTAGT 236
Db 194 GGAAGACAGGGGACCTTGGCGGCTTGGCGCTATCGAGCGGCGGATCTGTATGATAGCTGGT 253
Qy 237 TGGTGGGGTAAAGGCTTACCAAGGCAACGATCAGTAGTGTGCTCAGAGGACGACCAAGCC 296
Db 254 TGGCGGGTAAAGGCCCCCAAGCGGACGATCAGTAGCGGTCTGAGAGGATGATCCGCC 313
Qy 297 ACATCTGGGACTGAGACACGGGCCAGACTCTCTACGGGAGGACGAGTGGGGAAATTTGGAC 356
Db 314 ACATCTGGGACTGAGACACGGGCCAGACTCTCTACGGGAGGACGAGTGGGGAAATTTGGAC 373
Qy 357 AATGGCGAAGCCTGATCCAGCAATGCCGCTGAGTGNAGAAGG-CTTCGGGTGTGAAA 415
Db 374 AATGGCGCAAGCCTGATCCAGCCTATGCCGCTGTCTGAAGAAGGCTTTCGGGTGTGAAA 433
Qy 416 GCTCTTTTCAGTCGAGAAGAAAGTGTGACTAATAATCAAACTTATGATGTACCGAC 475
Db 434 GGACTTTTGTGACGGGAGAGAAAGGCTGTGTCATATACGGCGGCGATGACGTACTCTGA 493
Qy 476 AGAAGAAGCACCGGCTAACTACGTGCCAGCACCGCGGTAAATACGTAGGGTGCAAGCGTT 535
Db 494 AGAATAAGCACCGGCTAACTACGTGCCAGCACCGCGGTAAATACGTAGGGTGCGAGCGTT 553
Qy 536 AATCGGAATTAATCGGCGTAAGGGTGGCGAGCGGCTTTGTAAGTCAGATGTAATATCC 595
Db 554 AATCGGAATTAATCGGCGTAAGGGTGGCGAGCGGTTTACTTAAAGCAGGATGTGAAATCC 613
Qy 596 CCGGGCTTAACCTGGGAATTCGTTTGAAGCTACAAAGCTAGAGTGTAGCAGAGGGGGGT 655
Db 614 CCGGGCTTAACCTGGGAATTCGTTTGAAGCTAGAGTGTAGCAGAGGGGGGT 673
Qy 656 GGAATTCATGTGTAGCAGTGAATATGCGTAGAGATATGGAAGAACAATCGATGGCGAAGGC 715
Db 674 GGAATTCATGTGTAGCAGTGAATATGCGTAGAGATATGGAAGAACAATCGATGGCGAAGGC 733
Qy 716 AGCCCCCTGGGTAACTAGCTGCTCTACGAAAGCGGTGGGAGCAACAGGATTAAGA 775
Db 734 AGCCTCTGGGATAACACTGACGTTTCAATGCTCCGAAGCGTGGGTAGCAACAGGATTAAGA 793
Qy 776 TACCTGTGTAGTCCACGCGCTTAAACGATGTCAACTAGTGTGTGGGC-CTTACTAGGCTTG 834
Db 794 TACCTGTGTAGTCCACGCGCTTAAACGATGTCAATAGCTGTGTGGCAACTGTGTTGCTTG 853
Qy 835 GTAACTGATGTAACCGGTGAAGTTGACCGCTGGGGAGTAGCGGTGCGAGGATTAATAATC 894
Db 854 GTACGCTAGCTAAACCGGTGAAGTTGACCGCTGGGGAGTAGCGGTGCGAAGATTAATAATC 913
Qy 895 AAAGGAATTAAGCGGGACCCGCAACAGCGGTGGATATGTGGATTAATTCGATCAACGC 954
Db 914 AAAGGAATTAAGCGGGACCCGCAACAGCGGTGGATATGTGGATTAATTCGATCAACGC 973
Qy 955 GAAAAACCTTACCTACCTTGCATGTAGCGAATATTTTGAAGATTAATAATGTCCTTCG 1014
Db 974 GNAGAACCTTACCTTGTGTTTGCATGTGCGGAATCTCCGAGACGAGGAGTGCCTTCG 1033
Qy 1015 GGAACGCTTAAACAGGTGCTGATGGTGTGCTGATGCTGCTGATGATGTTGGGTGA 1074
Db 1034 GGAGCCGTAAACACAGGTGCTGATGGTGTGCTGATGCTGCTGATGATGTTGGGTGA 1093
Qy 1075 AGTCCGCAACAGCGGCAACCTTGTGATTAATTTGCCATCATTTAGTTGGGCACTTAAT 1134
Db 1094 AGTCCGCAACAGCGGCAACCTTGTGATTAATTTGCCATCATTTAGTTGGGCACTTAAT 1153
Qy 1135 GAGACTGCGGTGACAAACCGGAGGAGGTGGGATGACGTCAAGTCTCTCATGCGCCCTTA 1194

Db 1154 GAGACTGCGGTGACAAAGCCGAGGAGGTGGGGATGACGTCAAGTCTCTCATGCGCCCTTA 1213
Qy 1195 TGGGTAGGGCTTTCACAGTAATAAATGGCGCGTACAGAGGGTTGCCAACCCCGGAGGGG 1254
Db 1214 TGACACAGGGCTTTCACAGTCTATAAATGGTGGTACAGAGGGTAGCCAAAGCCGGAGCG 1273
Qy 1255 GAGCTAATCTCAGAAAGCGGTCTAGTCCGGATCGGAGTCTGCAACTCAGACTCCGTGAA 1314
Db 1274 GAGCAATCTCAGAAAGCGGTCTAGTCCGGATCGGATCGCACTCTGCAACTCAGAGTGA 1333
Qy 1315 GTCCGAATCTAGTAATTCGCGGATCAGCATGTCCGGTGAATACGTTCCCGGCTCTTGT 1374
Db 1334 GTCCGAATCTAGTAATTCGCGGATCAGCATGTCCGGTGAATACGTTCCCGGCTCTTGT 1393
Qy 1375 ACACACCGCGCTCAGCAACATGGGAGTGGGTTTCCAGAGAGCAGATAGTCTAACCGTAA 1434
Db 1394 ACACACCGCGCTCAGCAACATGGGAGTGGGGAATCCAGAGATAGTGGGTAAACCGGA 1453
Qy 1435 -GAGGGCGTTTGGCCACGCGGAGATTTCATGCTGG 1467
Db 1454 GGAAGTCCGCTTACCAACCGTATGCTTTCATGCTGG 1487

RESULT 5
US-09-735-567-4/c
; Sequence 4, Application US/09735567
; Patent No. 6608190
; GENERAL INFORMATION:
; APPLICANT: Bramucci, Michael
; TITLE OF INVENTION: Nucleic Acid Fragments for the Identification of Bacteria in
; TITLE OF INVENTION: Industrial Wastewater Bioreactors
; FILE REFERENCE: BC1033 US NA
; CURRENT APPLICATION NUMBER: US/09/735,567
; CURRENT FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/171,140
; PRIOR FILING DATE: 16 DECEMBER 1999
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 4
; LENGTH: 1453
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Dinitrifying bacteria
; OTHER INFORMATION: Nucleotide sequence of rDNA corresponding to strain RA2
US-09-735-567-4

Query Match 73.9%; Score 1084.8; DB 3; Length 1453;
Best Local Similarity 86.3%; Pred. No. 0;
Matches 1260; Conservative 0; Mismatches 187; Indels 13; Gaps 5;
Qy 12 TCAGATTGAACGCTGGCGGATGCTTTACATGCAAGTCAAGCGGAGCAGCGGTGCTT 71
Db 1453 TCAGATTGAACGCTGGCGGATGCTTTACATGCAAGTCAAGCGGAGCAGCGGTGCTT 1398
Qy 72 GCACCTGGTGGCGAGTGGCGGACGGGTGAGTATGATCGGACGTCGCAAGAGTGGG 131
Db 1397 CAACCTGGCGGAGCGGCGGAGTGAACATCGCAAGCGTCCGAGAGCGTGGG 1338
Qy 132 GATAACGCATCGAAGATGTCTAATACCGCATATCTCTACGGAGGAAAGCAGGGATC 191
Db 1337 GATAGCCCGGGAAGCGCGGATTAATACCGCATGATCTGAGGATGAAAGTGGGGAC 1278
Qy 192 GAAAGACCTTGTGCTTTTGGAGCGCGCATGCTGATAGTCTAGTGGTGGGTAAAGGC 251
Db 1277 GCAAGGCTCAACGCTTGGAGCGCGCATGCGGATAGTGTAGTGGTGGGTAAAGGC 1218
Qy 252 CTACCAAGGCAACGATCAGTGTGGTCTGAGGAGCAGCAGCAGCAGTGGGACTGGA 311
Db 1217 TTACCAAGCCTGGATCTGTAGTGGTCTGAGAGGATGATCAGCAGCAGTGGGACTGGA 1158
Qy 312 CACGGCCAGACTCTCTACGGGAGCGAGTGGGGAATTTTGGACAATGGCGAAGCCT 371

Db 1157 CACGGCCACAGCTCCACGCGGAGGCGAGCGAGTGGGAAATTTTGGCAATGGGGCGCAGCCT 1098
Qy 372 GATCCAGCAATGCGGGTGAGTGAAGAAGG-C TTTCGGGTGTGAAGCTCTTTCAGTTCGAG 430
Db 1097 GATCCAGCAATGCGGGTGAGGAGCGAGGAGGCTTCGGGTGTGAAGCTCTTTCAGCGA 1038
Qy 431 AAGAAAGGTTGTGACTAATAATACAACTTATGATGGTACGACAGAGAGACCGGC 490
Db 1037 ACGAAAGGCTCTCTTAATACAGGGGGCATATGACGGTACCGTAAAGATAAGCACCAGC 978
Qy 491 TAACTAGTGCAGACGCGCGGTAAATACGTAAGTGTGCAAGCGTTAATCGGAATTAAGTGG 550
Db 977 TAACTAGTGCAGACGCGCGGTAAATACGTAAGTGTGCAAGCGTTAATCGGAATTAAGTGG 918
Qy 551 GCGTAAAGGTTGCGAGCGCGCTTTGTAAGTGTGCAAGTGAATCCCGGGCTTAACTGG 610
Db 917 GCGTAAAGGTTGCGAGCGCGCTTTTGAAGACAGAGTGAATCCCGGGCTCAACTGG 858
Qy 611 GAATTCGTTTGAACCTACAAAGCTAGAGTGTAGCAGAGGGGTGGAATTCATGTGTGA 670
Db 857 GAATTCGTTTGTACTGTGCAAGCTGTAGTGTGCGCAGAGGGGATGGAATTCGCGGTGA 798
Qy 671 GCAGTGAATCGTAGAGATATGGAAGAAATCGATGCGAAGCGACGCCCTCGGGTTAA 730
Db 797 GCAGTGAATCGTAGATATGCGGAGGAAACACCGATGCGAAGGCAATCCCTGGGCTG 738
Qy 731 CACTGACGCTATGACAGAAAGCTGGGAGCAACAGGATTAGATACCTCGGTAGTCCA 790
Db 737 CACTGACGCTATGACAGAAAGCTGGGAGCAACAGGATTAGATACCTCGGTAGTCCA 678
Qy 791 CGCCCTAAACGATGCAACTAGTTGTTGGGCTTACTAGGCTTGGTAACTGAGTAAACGC 850
Db 677 CGCCCTAAACGATGCAACTAGTTGTTGGGAAATTCATTTCTCAGTAAACGAAAGCTAACGC 618
Qy 851 GTGAAGTTGACCGCTGGGAGTAGCGTGCAGGATTAATACTCAAGGAAATTCAGCGGG 910
Db 617 GTGAAGTTGACCGCTGGGAGTAGCGCGCGAAGGTTAAACTCAAGGAAATTCAGCGGG 558
Qy 911 ACCGCAAGCGGTGGAATTAATGGAATTAATGATGCAACGCGGAAAACTTTACTTAC 970
Db 557 ACCGCAAGCGGTGGAATTAATGGAATTAATGATGCAACGCGGAAAACTTTACTTAC 498
Qy 971 CTTGACATGTAGCGAAATATTTAGAGATAAATAGTG--CCTTCGGAAAGCTTAACACA 1028
Db 497 TTTTGACATGTAGCGAAATCTCAGAGACGCGAGGAGTGCTCGAAAGAGAGCGGTAAACACA 438
Qy 1029 GGTGCTGCATGCTGCTCAGCTCGTGTGAGATGTTGGGTTAAGTCCCGCAACGAG 1088
Db 437 GGTGCTGCATGCTGCTCAGCTCGTGTGAGATGTTGGGTTAAGTCCCGCAACGAG 378
Qy 1089 CGCAACCTTGTATTAAATGTCATCATTTAGTGGGCACTTTAATGAGATGCGCGTGA 1148
Db 377 CGCAACCTTGTATTAGTTGTTGTCAGA-----AAGGGCACTCTAATGGGACTGCCGGTGA 323
Qy 1149 CAAACCGGAGGAGTGGGAGTGAAGTCAAGTCTCATGCGCCCTTATGGTAGGCTTCA 1208
Db 322 CAAACCGGAGGAGTGGGAGTGAAGTCAAGTCTCATGCGCCCTTATAGTGGGCTTCA 263
Qy 1209 CAGTAAATCAATGGCGGTACAGAGGGTTGCAACCCGCGAGGGGAGCTAATCTCAGA 1268
Db 262 CAGTAAATCAATGGCTGTGTACAAAGGTTGCCAACCCGCGAGGGAGCCCAATCCACA 203
Qy 1269 AAGCGGCTGTAGTCCGAGTCCGAGTCTCGAATCGCTCGTGAAGTGGGAATCGCTAG 1328
Db 202 AAGCGGCTGTAGTCCGAGTCCGAGTCTCGAATCGCTCGTGAAGTGGGAATCGCTAG 143
Qy 1329 TAATCGGATCAGATGTGCGGTGCAATACAGTTCCCGGCTCTTGTACACACCGCCCGTC 1388
Db 142 TAATCGGATCAGATGTGCGGTGCAATACAGTTCCCGGCTCTTGTACACACCGCCCGTC 83
Qy 1389 ACACCATGGAGTGGGTTTCCAGAGCGAGTAGTCTAACCGTAA--GAGGGGTTGGC 1447

Db 82 ACACCATGGGAGCGGGTTCTGCCAGAAAGTAGTTAGCCTAACCCGAGGAGGGCGATTACC 123
Qy 1448 ACGCGAGGATTCATGACTGG 1467
Db 22 ACGGAGGGTTCTGACTGG 3
RESULT 6
US-08-642-229A-3
; Sequence 3, Application US/08642229A
; Patent No. 5974291
; GENERAL INFORMATION:
; APPLICANT: Herwig, Russell P.
; APPLICANT: Bielefeldt, Angela R.
; APPLICANT: Stensel, H. David
; APPLICANT: Strand, Stuart E.
; TITLE OF INVENTION: Degradation of Environmental Toxins by a
; TITLE OF INVENTION: Filamentous Bacterium
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christensen O'Connor Johnson and Kindness PLLC
; STREET: 1420 Fifth Avenue, Suite 2800
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: WA 98101-2347
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/642,229A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/246,865
; FILING DATE: 20-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sheiness, Diana K.
; REGISTRATION NUMBER: 35,356
; REFERENCE/DOCKET NUMBER: UOFW19233
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 682 8100
; TELEFAX: (206) 224 0779
; TELEX: 4938023
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1455 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: nucleic acid
; DESCRIPTION: "16S ribosomal DNA"
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Unknown. Possibly new species
; STRAIN: A-1
; US-08-642-229A-3

Query Match 73.7%; Score 1081.6; DB 2; Length 1455;
Best Local Similarity 86.6%; Pred. No. 0;
Matches 1262; Conservative 1; Mismatches 182; Indels 13; Gaps 6;
Qy 16 ATTGAACGCTGGCGGCGATGCTTTTACATCATCAAGTCGAAACGGGAGCAGCGGTGCTTCAC 75
Db 1 ATTGAACGCTGGCGGCGATGCTTTTACATCATCAAGTCGAAACGGGAGCAGCGGTGCTTCAC 58
Qy 76 CTGTGGGAGTGGCGGACCGGTGAGTAATGCAATCGGAACTGTCAGAAAGTGGGGGATA 135
Db 59 CTGATGGCGAGTGGCGGAAACGGGTGAGTAATACATCGGAACTGTCCTGTAGTGGGGGATA 118

[illegible]

Db 1445 ACTGG 1449

RESULT 8
US-09-617-854A-1
; Sequence 1, Application US/09617854A
; Patent No. 6461840
; GENERAL INFORMATION:
; APPLICANT: BRAMUCCI, MICHAEL G.
; APPLICANT: MCCUTCHEN, CAROL M.
; APPLICANT: NAGARAJAN, VASANTHA
; APPLICANT: THOMAS, STUART M.
; TITLE OF INVENTION: Microbial Production of Terephthalic Acid and
; TITLE OF INVENTION: Isophthalic Acid
; FILE REFERENCE: CL-1257
; CURRENT APPLICATION NUMBER: US/09/617,854A
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/091,645
; PRIOR FILING DATE: JULY 2, 1998
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 1
; LENGTH: 1451
; TYPE: DNA
; ORGANISM: Burkholderia sp.
US-09-617-854A-1

Query Match 73.5%; Score 1078.2; DB 3; Length 1451;
Best Local Similarity 86.0%; Pred. No. 0;
Matches 1243; Conservative 0; Mismatches 193; Indels 9; Gaps 4;

QY	26	GGCGGCATGCTTTACACATCGAAAGTCGAAACGGCAGCAGCGGTGCTTGGACCTGTGTGGCGA	85
DB	11	GGCGCATGCTTTACACATCGAAATTCAAACGGCAGCAGCGGTGCTTGGACCTGTGTGGCGA	70
QY	86	GTGCGGACGGGTGAGTAATGCATCGGAACTGTCAGAAAGTGGGGGATACGCATCGAA	145
DB	71	TTGCGGAAACGGGTGATTAATACATCGGAAATGTACTCTGTAGTGGGGATACCTCGGCANA	130
QY	146	AGATGTGCTAATACCGCATATTCCTACGAGGAGAAAGCAGGGGATCGAAAGACTTTGTGC	205
DB	131	AGCGGATTAATACCGCATACGCTCTCAGGAGGAAAGCGGGGACCTTCGGGCTTCGCGC	190
QY	206	TTTTGGAGCGGCGCATGCCTGATTAGCTAGTTTGTGTGGGTAAAGCCCTACCAAGGCAACG	265
DB	191	TACAAAAGCAGCGCATGTCAAAATACCTATTTGTGTGGGTAAAGCTCACCCAGCGACA	250
QY	266	ATCAGTAGTTGGTCTGAGAGAGCACACGACACTGGGACTGAGACACGCGCCAGATCC	325
DB	251	ATCTGTACTGCTCTGAGAGCAACACCCACACTGGGACTGGAACACGCGCCAAACTC	310
QY	326	CTACGGGAGGCGAGTGGGGAAATTTTGGACAATGGGGGAAAGCCTGATCCAGCAATGCC	385
DB	311	CTACGGGAGGCGAGTGGGGAAATTTTGGACAATGGGGGAAAGGCTGATCCACCAATGCC	370
QY	386	CGGTGAGTGAAGAGG-CTTCGGGTGTAAAGCTCTTTTCACTCAGAGAAGAAAGGTTCTGT	444
DB	371	CGGTGTGTGAAGAGGCTTCGGGTGTAAAGCACTTTTGTCCGGAAGAAATCCTCTGG	430
QY	445	ACTAATATCAACAATTATGATGTGTCGACAGAGAAGACACCGGCTAACTACGTGCCAG	504
DB	431	GTTAATATCTCGGGGGATACGCTACCGGAAAAATAAGCACCGGCTAACTACTTGGCA-	489
QY	505	CAGCCGGGTAAATACGTAGGTGCAGAGGTTAATCGGAATTACTTGGGCGTAAAGGGTCCG	564
DB	490	CAGCCGGGTAAATCTTAGGTGCAGAGGTTAATCGGAATTACTTGGGCGTAAAGCGTCCG	549
QY	565	CAGGGCGCTTTGTAAGTCAGATGTGAATCCCGGGCTTAACTCTGGGAAATTCGCTTGAA	624
DB	550	CAGGGCGCTTTGTAAGACGGATGTGAATCCCGGGCTTAACTCTGGGAACTGCATTCGT	609
QY	625	ACTACAAAGCTAGAGTGTAGCAGAGGGGGTGGAAATTCATGTGTAGCAGTGAATCGGT	684

Db 610 ACTGACAGCTAGATATGGCAGAGGGGGTAGAATTCACGCTGTAGCAGTGAATCGCT 669
Qy AGAGATATGGAGACATCGATGGCGAAGGAGCGCCCTGGTTAACTACAGCTCATG 744
Db 670 AGAGATATGGAGACATCGATGGCGAAGGAGCGCCCTGGTTAACTACAGCTCATG 729
Qy 745 CACGAAACGCTGGGAGCAACAGGATTAGATACCTTGGTATGCCAGCCCTAAACGATG 804
Db 730 CACGAAACGCTGGGAGCAACAGGATTAGATACCTTGGTATGCCAGCCCTAAACGATG 789
Qy 805 TCAACTAGTTGTTGGCCCTTACTAGGCTTGTAGCTAGCTAAACGCTGAAGTTGACCGC 864
Db 790 TCAACTAGTTGTTGGGCTTCAATTCCTTAGTAAACGAGCTAAACGCTGAAGTTGACCGC 849
Qy 865 CTGGGAGTACGCTGCGAGGATTAACCTCAAGGAATTGACGGGACCCGACAGCGG 924
Db 850 CTGGGAGTACGCTGCGAGGATTAACCTCAAGGAATTGACGGGACCCGACAGCGG 909
Qy 925 TGGATTATGTGGATTAAATTCGATGCAACGCGGAAACCTTACCTTACCATGTAGC 984
Db 910 TGGATTATGTGGATTAAATTCGATGCAACGCGGAAACCTTACCTTACCATGTAGC 969
Qy 985 GAATATT--TTAGAGATAAATATAGTGCCTTCGGGAAACGCTAACACAGCTGTGATGCT 1042
Db 970 GAATCTTGTCTGAGAGGTGAGAGTGTCTCGAAAGAGAAACGCTAACACAGCTGTGATGCT 1029
Qy 1043 GTCGTCAGCTGCTGCTGAGATGTTGGTTAACTGCTGCGGAAACGCTAACACAGCTGTGATGCT 1102
Db 1030 GTCGTCAGCTGCTGCTGAGATGTTGGTTAACTGCTGCGGAAACGCTAACACAGCTGTGATGCT 1089
Qy 1103 TTAATTGTCATCAATTTAGTTGGGCACTTTAATGAGACTGCGGCTGACAAACGCGGAGG 1162
Db 1090 TTAGTTGCTACGCA--GAGCACTCTAAGGAGACTGCGGCTGACAAACGCGGAGG 1144
Qy 1163 GTGGGATGACGTCAGCTCAATGCTTATGGTTAGGCTTACACGTAATCAATG 1222
Db 1145 GTGGGATGACGTCAGCTCAATGCTTATGGTTAGGCTTACACGTCATACATG 1204
Qy 1223 GCGGTTACAGAGGTTGCCAACCGCGGAGGGAGCTTAATCTCAGAAAGCGCTGATG 1282
Db 1205 GTCGTTACAGAGGTTGCCAACCGCGGAGGGAGCTTAATCTCAGAAAGCGCTGATG 1264
Qy 1283 CCGGATCGGAGTCTGCAACTCGACTCCGTTGAAGTCCGAAATCGCTAGTAATCGCGGATCAG 1342
Db 1265 CCGGATCGGAGTCTGCAACTCGACTCCGTTGAAGTCCGAAATCGCTAGTAATCGCGGATCAG 1324
Qy 1343 CATGTCGGGTGAATAGCTTCCCGGCTTCTTACACACCGCCGCTCACACCATGGAGTG 1402
Db 1325 CATGTCGGGTGAATAGCTTCCCGGCTTCTTACACACCGCCGCTCACACCATGGAGTG 1384
Qy 1403 GGTTCACAGAGCAGATAGCTTAACCGTTAAGAGGGGTTGTCACCGGCGAGATTATG 1462
Db 1385 GGTTCACAGAGCAGATAGCTTAACCGTTAAGAGGGGTTGTCACCGGCGAGATTATG 1444
Qy 1463 ACTGG 1467
Db 1445 ACTGG 1449

RESULT 9

US-08-642-229A-2
; Sequence 2, Application US/08642229A
; Patent No. 5874291
; GENERAL INFORMATION:
; APPLICANT: Herwig, Russell P.
; APPLICANT: Bielefeldt, Angela R.
; APPLICANT: Stensel, H. David
; APPLICANT: Strand, Stuart E.
; TITLE OF INVENTION: Degradation of Environmental Toxins by a
; TITLE OF INVENTION: Filamentous Bacterium
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christensen O'Connor Johnson and Kindness PLLC

STREET: 1420 Fifth Avenue, Suite 2800
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: WA 98101-2347
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/642,229A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/246,865
FILING DATE: 20-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sheiness, Diana K.
REGISTRATION NUMBER: 35,356
REFERENCE/DOCKET NUMBER: UOFW19233
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682 8100
TELEFAX: (206) 224 0779
TELEX: 4938023
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1452 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: nucleic acid
DESCRIPTION: "16S ribosomal DNA"
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Brachyomonas denitrificans AS-P1
US-08-642-229A-2

Query Match 72.7%; Score 1066.8; DB 2; Length 1452;
Best Local Similarity 85.6%; Pred. No. 0;
Matches 1247; Conservative 0; Mismatches 197; Indels 12; Gaps 5;

Qy 16 ATTCAACGCTGGCGGCATGCTTTACATCAATCAAGTCGAAACGCGAGCAGCGGTGCTTGAC 75
Db 1 ATTCAACGCTGGCGGCATGCTTTACATCAATCAAGTCGAAACGCGAGCAGCGGTGCTTGAC 57
Qy 76 CTGCTGGCGAGTGGCGGACGCGGTGAGTAATGTCATCGGAACGCTGCCAGAGTGGGGGATA 135
Db 58 ATGCTGACGAGTGGCGAAGCGGTGAGTAATGTCATCGGAACGCTGCCAGAGTGGGGGATA 117
Qy 136 AGCATCGAAAGATGCTCTAATACCGCATATTTCTACGAGGAGAAACGAGCGGATCGAAA 195
Db 118 ACTACTCGAAAGAGTGGCTAATACCGCATGAGAACTGAGGTTGAAAGCGGGGACCTTTG 177
Qy 196 GACCTTGTCTTTTGGAGCGCGCATGCTGATTAGCTAGTTGTTGGGTAAGGCGCTTAC 255
Db 178 GGCCTCGCGCTACTGGAGCGCGCATATCAGATTAGTTGGGTAAAGCGCTTAC 237
Qy 256 CAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCGACCATCTGGGATCTGAGACACG 315
Db 238 CAAGCCGACGATCTGTAGCTGGTCTGAGAGGACGACCGACCATCTGGGATCTGAGACACG 297
Qy 316 GCCCAGACTCTACCGGAGGACGAGTGGGGAATTTTGGACATGGGGGAAAGCTGATC 375
Db 298 GCCCAGACTCTCTACCGGAGGACGAGTGGGGAATTTTGGACATGGGGAAGCTGATC 357
Qy 376 CAGCAATGCCGCTGAGTGAAGAGG--CTTCGGGTTGTAAAGCTCTTTTACGTCGAGAGA 434
Db 358 CAGCAATGCCGCTGAGTGAAGAGGCTTCGGGTTGTAAAGCTCTTTTACGTCGAGAGA 417
Qy 435 AAAGTTGTGACTAATAATCAACTTATGATGTTACCGACAGAGGACGACCGGCTAAC 494

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Db 418 AAGGCTCTGTTAATACCTGGGCTCATGACGGTACTGTAAAGATAAGACCGGCTAAC 477
Qy 495 TACGTGCAGCAGCGCGGTAATACTAGGTGCAAGCGTTAATCGGAATTAATCTGGCGGT 554
Db 478 TACGTGCAGCAGCGCGGTAATACTAGGTGCGAGCGTTAATCGGAATTAATCTGGCGGT 537
Qy 555 AAGGGTCCGACGCGCTTTGTAAAGTCAGATGTAAGTAAATCCCGGGCTTAACCTGGGAAT 614
Db 538 AAGCGTCCGACGCGCTTTGTAAAGTCAGATGTAAGTAAATCCCGGGCTTAACCTGGGAAC 597
Qy 615 TGGCTTTGAACACTCAAGCTAGAGTGTACGAGGGGGTGGAAATCCATGTGTAGCAG 674
Db 598 TGCATTGGTGACTCAAGGCTGGAGTGGCGAGAGGGGGATGGAAATCCCGGTGTAGCAG 657
Qy 675 TGAATGCGTAGAGATATGAAGAAACATCGATGGCGAAGGCGCCCTCGGTAAACACT 734
Db 658 TGAATGCGTAGATATGCGGAGGAACACCGATGCGAAGCAATCCCTCGGCTGCACT 717
Qy 735 GACGCTCATGCAAGAAAGCGTGGGAGCAACAGGATTAGATACCTGGTAGTCCAGCC 794
Db 718 GACGCTCATGCAAGAAAGCGTGGGAGCAACAGGATTAGATACCTGGTAGTCCAGCC 777
Qy 795 CTAACGATGTCAACTAGTGTGGGCTTACTAGGCTTGTAACTAGCTTAACGCTGA 854
Db 778 CTAACGATGTCAACTAGTGTGGGTATTTGCTTACTGATGAAGCTTAACGCTGA 837
Qy 855 AGTTGACCGCTGGGAGTACGCTCGCAGGATTAATACTCAAGGAATTAACCGGGACCC 914
Db 838 AGTTGACCGCTGGGAGTACGCTCGCAGGATTAATACTCAAGGAATTAACCGGGACCC 897
Qy 915 GCACAAGCGGTGATATGTGGATTAATTCGATGCAAGCGGAAACCTTACCTACCTT 974
Db 898 GCACAAGCGGTGATATGTGGTAAATTCGATGCAAGCGGAAACCTTACCTACCTT 957
Qy 975 GACATGTAGCAATATTTTACAGATATAATAGT - CCTTCGGAAGCGCTAAACAGGTG 1032
Db 958 GACATGTAGCAATATTCGAAAGATTTGGAAGTCTCGTAAGAGAACTGCAACAGGTG 1017
Qy 1033 CTGATGCGCTGCTGAGCTGCTGCTGAGATGTTGGGTAAAGTCCCGCAACGAGCGCA 1092
Db 1018 CTGATGCGCTGCTGAGCTGCTGCTGAGATGTTGGGTAAAGTCCCGCAACGAGCGCA 1077
Qy 1093 ACCCTTGCATTAATGCGCATTAATGTTGGGCACTTAAATGAGACTGCCGCTGACAAA 1152
Db 1078 ACCCTTGCATTAATGTTGCTACA - - - - - AAGGGCACTCTAATGGGACTGCCGCTGACAAA 1132
Qy 1153 CCGAGGAAGGTGGGATGAGCTCAAGTCTCATGGCCCTTATGGTAGGGCTTTCACAG 1212
Db 1133 CCGAGGAAGGTGGGATGAGCTCAAGTCTCATGGCCCTTATAGGTGGGCTACACAG 1192
Qy 1213 TAATAAATGGCGGTACAGAGGTTGCAACCCGCGAGGGGAGCTTAATCTCAGAAAGC 1272
Db 1193 TCATAAATGGCGGTACAAAGGGTAGCAACCCGCGAGGGGAGCCAAATCCCAATAAGC 1252
Qy 1273 GCGTGTAGTCCGATCGGAGTCTGCAACTGCACTCCGTGAAGTCGGAATCGTAGTAAT 1332
Db 1253 CCGTGTAGTCCGATCGGAGTCTGCAACTGCACTCCGTGAAGTCGGAATCGTAGTAAT 1312
Qy 1333 CCGGATCAGCATGTCGGGTGAATACGTTCCCGGGTCTTGTACACACCGCCGCTCACAC 1392
Db 1313 CCGGATCAGCATGTCAGGTGAATACGTTCCCGGGTCTTGTACACACCGCCGCTCACAC 1372
Qy 1393 CATGGAGTGGGTTTCAACAGAGCAGATAGTCTTAACCGTTAA - GAGGGCGTTTGGCAGG 1451
Db 1373 CATGGAGCGGTTCTGCGCAGAAAGTGGTTAGCTTAACCGTTAAGGAGGCGATCAACAGG 1432
Qy 1452 CGAGATTCACTGCTGG 1467
Db 1433 CAGGTTCTGCTGCTGG 1448

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RESULT 10

US-09-063-898-1

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; Sequence 1, Application US/09063898
; Patent No. 6319497
; GENERAL INFORMATION:
; APPLICANT: Casida, Jr., Lester E.
; APPLICANT: Falkinham, III, Joseph Oliver
; APPLICANT: Cain, Cody C.
; TITLE OF INVENTION: NON-OBLIGATE PREDATORY BACTERIUM
; TITLE OF INVENTION: BURKHOLDERIA CASIDAE AND USES THEREOF
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1667 K Street, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/063,898
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: 60/044,532
; APPLICATION NUMBER: 60/044,532
; FILING DATE: 23-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 8743-006-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)7909090
; TELEX: 66141 PENNIE
; TELEFAX: (212)8699741
; INFORMATION FOR SEQ ID NO: 1:
; LENGTH: 1495 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: Genomic DNA
; US-09-063-898-1

Query Match 71.9%; Score 1054.6; DB 3; Length 1495;
Best Local Similarity 86.7%; Pred. No. 0;
Matches 1267; Conservative 0; Mismatches 179; Indels 15; Gaps 9;

Qy 14 AGATTGAACGCTGGCGCATGCTTTTACA-CATGCAAGTCGAACGGCAGCAGCGGTGCTTG 72
Db 1 AATATTACGCTGGTTGCATGCCCTTACAGCATCAAGTCGNAACGGCAGCAGCGGTGCTTG 60
Qy 73 CACTGTGTGCGAGTGGCGGACGCGGTGAGTAATGCAATCGGAAC-GTGTCCAGAGTGGG 131
Db 61 CACTGTGTGCGAGTGGCGGAAACGCGGTGAGTAATACATCGGAACAATGCTGTAGTGGG 120
Qy 132 GATAACGCAATCGAAGATGTCTAATACCGCATATTTCTACGAGGAAAGCAGGCGATC 191
Db 121 GATAGCCCGCGAAGCGGATTAATACCGCATACGATCTACGATGAAGCGGCGGAC 180
Qy 192 GAAAGACTTGTGTCTTTTGGAGCGGCGGATGCTCTGATTAGCTAGTGGGTAAAGGC 251
Db 181 TTCCGGGCTCGCGCTATAGGTTGGCGGATGGCTGATTAGTGTGGGTAAAGGC 240
Qy 252 CTACCAAGGCAACGATCAGTAGTGTCTGAGAGGACGACAGCCACACTGGGACTGAGA 311
Db 241 CTACCAAGGCGAGGATCAGTAGTGT-GTCTGAGAGGACGACGACCACTGGGACTGAGA 299
Qy 312 CAGGCGCCAGACTCCTACGGGAGGCGACGAGTGGGGAATTTTGGACAAATGGGCGAAAGCCT 371
Db 300 CAGGCGCCAGACTCCTACGGGAGGCGACGAGTGGGGAATTTTGGACAAATGGGCGAAAGCCT 359

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Qy 252 CTACCAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACAGCCACATCGGAGCTGAGA 311
Db 241 CTACCAAGGCGACGATCAGTAGTT-GTCTGAGAGGACGACAGCCACATCTGGAGCTGAGA 299
Qy 312 CAGGGCCGACACTCTTACGGGAGGCGACAGTGGGGAATTTTGACATGGCGGAAGCCT 371
Db 300 CAGGGCCGACACTCTTACGGGAGGCGACAGTGGGGAATTTTGACATGGCGGAAGCCT 359
Qy 372 GATCCAGCAATGCCGCTGAGTGAAGAAGG-CTTCGGGTTGTAAAGCTCTTTTCAGTCTGAG 430
Db 360 GATCCAGCAATGCCGCTGAGTGAAGAAGGCTTCGGGTTGTAAAGCACATTTTGTCCGGA 419
Qy 431 AAGAAAGGTTGTGACTAATAATCACAACTTATGATGGTACCGACAGAAAGACCCGGC 490
Db 420 AAGAAATCCTTTGGTTCTTAATATAGCCGGGGATGACGGTACCGGAAGAAATAAGCACCGGC 479
Qy 491 TNACTAGTGCACGACGCGGGTAAATACGTAGGGTCCGAGCGGTTAATCGGAATTACTGG 550
Db 480 TNACTAGTGCACGACGCGGGTAAATACGTAGGGTCCGAGCGGTTAATCGGAATTACTGG 539
Qy 551 GCGTAAAGGGTGCACGCGGCTTTGTAAGTTCAGATGTGAATCCCCGGGCTTAAACCTGG 610
Db 540 GCGTAAAGCGTGCACGCGGCTTTGCTAAGCCGATGTGAATCCCCGGGCTCAAACCTGG 599
Qy 611 GAATTGCGTTGAACTACAAGCTAGAGTGTAGCAGAGGGGGTGAATTCATGTGTA 670
Db 600 GAACTGCAATGGTGACTGGCAGGCTAGAGTATGCGAGGGGGGTAGAATTCACAGTGA 659
Qy 671 GCAGTGAATGCGTAGAGATATGAAGCAATCGATGCGGAGGCGAGCCCTGGGTTAA 730
Db 660 GCAGTGAATGCGTAGAGATATGAAGCAATACCGATGCGGAGGCGAGCCCTGGGCGAA 719
Qy 731 CACTGACGCTCATGCACGAAAGCGTGGGAGCAAAACAGGATTAGATACCCTGTGTAGTCCA 790
Db 720 TACTGACGCTCATGCACGAAAGCGTGGGAGCAAAACAGGATTAGATACCCTGTGTAGTCCA 779
Qy 791 CGCCCTAAACGATGCAACTAGTTGTTGGGCTTACTAGGTTGGTAAAGCTAGCTAACGC 850
Db 780 CGCCCTAAACGATGCAACTAGTTGTTGGGGAATTCATTTCTTAGTAACGTTAGCTAACGC 839
Qy 851 GTGAAGTTGACCGCTCGGAGTACGCTCGCAGGATTTAAACTCAAAGGAATTCGACGGG 910
Db 840 GTGAAGTTGACCGCTCGGAGTACGCTCGCAGGATTTAAACTCAAAGGAATTCGACGGG 899
Qy 911 ACCGCGACAAAGCGTGGATTAATGTTGATTAATTCGATGCAACGCGAAGAACTTACCTAC 970
Db 900 ACCGCGACAAAGCGTGGATTAATTCGATGCAACGCGAAGAACTTACCTAC 959
Qy 971 CTTTGAATGAGCGAAT--ATTTTAGAGATAAAATAGTCCTTCGGGAGCGCTTAACACA 1028
Db 960 CTTTGAATGAGCGAATCCCGCTGAGAGTGGGAGTGCTCGAAGAGAACTCCGCGCACA 1019
Qy 1029 GGTCTGCATGGCTGCTCAGCTCGTGTCTGTAGATGTTGGGTTAAGTCCCGCAACGAG 1088
Db 1020 GGTCTGCATGGCTGCTCAGCTCGTGTCTGTAGATGTTGGGTTAAGTCCCGCAACGAG 1079
Qy 1089 CGCAACCTTGTCAATTAATTTGCCATCAATTTAGTTGGGCACTTTTAATGAGACTGCGGTGA 1148
Db 1080 CGCAACCTTGTCTTGTGCTACGCAAGA-----GCATCTTAAGGAGACTGCGCGTGA 1134
Qy 1149 CAACCGGAGGAGGTGGGATGACGTCAAGTCTCATGGCCCTTATGGGTAGGGCTTCA 1208
Db 1135 CAACCGGAGGAGGTGGGATGACGTCAAGTCTCATGGCCCTTATGGGTAGGGC-TCA 1193
Qy 1209 CACGTAATACAACTCGCGTACAGAGGTTGCCAAACCGCGAGGGGAGCTAATCTCAGA 1268
Db 1194 CACGTCATACAACTGTCGGAACAGAGGGTTGCC-ACCGCGAAGGGGAGCTAATCCCAGA 1252
Qy 1269 AAGCGCGTGTAGTCCGATCGGAGTCTGCAACTCGACTCCGTAAGTTCGGAATCGGTAG 1328
Db 1253 AAACCGGATCGTAGTCCGATTCGACTCTGCACTCGAGTGCAATGAAGCTGGAATCGGTAG 1312
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Qy 1329 TAATCCGGATCAGCATGTCGGGTGAATACGTTCCGGGTCTTTGTACACACGCCCGTC 1388
Db 1313 TAATCCGGATCAGCATGTCGGGTGAATACGTTCCGGGTCTTTGTACACACGCCCGTC 1372
Qy 1389 ACACCATGGAGTGGGTTTCCACAGAAAGCAGATAGTCTAACCCGTAAG--AGGGCGTTTGC 1446
Db 1373 ACACCATGGAGTGGGTTTACCAAGAAAGTGGCTAGTCTAACCCGCAAGGAAGACGGTCCC 1432
Qy 1447 CACGGCGAGATTCACTGCTGG 1467
Db 1433 CACGGTAGGATTCACTGACTGG 1453

RESULT 12
US-09-735-567-2/c
; Sequence 2, Application US/09735567
; Patent No. 6608190
; GENERAL INFORMATION:
; APPLICANT: Bramucci, Michael
; TITLE OF INVENTION: Nucleic Acid Fragments for the Identification of Bacteria in
; FILE OF INVENTION: Industrial Wastewater Bioreactors
; FILE REFERENCE: BC1033 US NA
; CURRENT APPLICATION NUMBER: US/09/735,567
; CURRENT FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/171,140
; PRIOR FILING DATE: 16 DECEMBER 1999
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 2
; LENGTH: 1467
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Brachymonas
; OTHER INFORMATION: Nucleotide sequence of 16S rDNA corresponding to strain NBYE13
US-09-735-567-2

Query Match 71.5%; Score 1049.2; DB 3; Length 1467;
Best Local Similarity 85.2%; Pred. No. 0;
Matches 1244; Conservative 0; Mismatches 203; Indels 13; Gaps 6;

Qy 14 AGATTGAACGCTCGCGCATGCTTTACACATGCAAGTCGAACCGGACGACCGGTGCTTGC 73
Db 1467 AGATTGAACGCTCGCGCATGCTTTACACATGCAAGTCGAACCGGACG-CCGCTCTTCG 1410
Qy 74 ACCTGTGGCGATGCGGACGCGGTGAGTAAATCATCGNAACGTGTCAGAACTGGGGGA 133
Db 1409 GGAATGGCGCGAGTGGCGAACCGGTGAGTAAAGCATCGGAACGTGCCCGGTAGTGGCGGA 1350
Qy 134 TAACGCATCGAAGATGTGCTAATACCGCATATTCCTACGGAGGAAGACAGGGGA--TC 191
Db 1349 TAGCTCGGCGAAGCGCGGATTAATACCGCATGAGATCCGTTGATGAAGACAGGGACTCG 1290
Qy 192 GAAAGACCTTGTCTTTTGGAGCGCGCATGCTGATTTAGCTAGTTGGTGGGTAAAGGC 251
Db 1289 CAAGGGCTTGGCTACTCGAGCGCGCATGTCCAGATTAGGTAGTTGGTGGGTAAAGGC 1230
Qy 252 CTACCAAGGCAACGATCAGTAGTTGTTCTGAGAGGACGACAGCCACACTGGGACTGAGA 311
Db 1229 CCACCAAGCTCGGATCTGTAGCTGGTCTGAGAGGATGATCAGCCACATCGGGACTGAGA 1170
Qy 312 CAGGGCCGACACTCTTACGGGAGGCGAGCTGGGGAATTTTGACATGGCGGAAGCCT 371
Db 1169 CAGGGCCGACACTCTTACGGGAGGCGAGCTGGGGAATTTTGACATGGCGGAAGCCT 1110
Qy 372 GATCCAGCAATCGCGGTGAGTGAAGAAGG-CTTCGGGTTGTAAAGCTCTTTTCAGTCTGAG 430
Db 1109 GATCCAGCAATCGCGGTGAGTGAAGAAGCCTTCGGGTTGTAAAGCTCTTTTCAGTCTGAG 1050
Qy 431 AAGAAAGGTTGTGACTTAATAATCAACNACTTATGATGGTACCGACAGAAAGCACCGGC 490
Db 1049 ACGAAAGGGCTCTTTCTTAATAAAGAGGGGCATGACCGGTACCGTAAAGCAATTAAGCACCGGC 990
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Qy 491 TAACTACGTGCGCAGCGCGGTAAATACGTAGGTCGAAGCGTTAAATCGGAATTAACCTGG 550
Db 989 TAACTACGTGCGCAGCGCGGTAAATACGTAGGTCGAAGCGTTAAATCGGAATTAACCTGG 930
Qy 551 GGTAAAGGGTGGCAGCGCGGTGGTAAAGTCAGATGTAATCCCGGGCTTAACCTGG 610
Db 929 GGTAAAGGGTGGCAGCGCGGTGGTAAAGTCAGATGTAATCCCGGGCTTAACCTGG 870
Qy 611 GAAATGGCTTTGAAACTACAAGCTAGAGTGTAGCAGAGGGGGTGGAAATTCCTATGCTGA 670
Db 869 GAACTGCCATTTGTGACTGCAAGCTGGAGTACCGCAGAGGGGGTGGAAATTCCTATGCTGA 810
Qy 671 GCAGTGAATCGGTAGAGATATGGAAGAACATCGATGGCGAAGCGAGCGCCCTGGGTTAA 730
Db 809 GCAGTGAATCGGTAGATATGCGGAGGAACACCGATGGCGAAGCGAGTCCCTGGGCTG 750
Qy 731 CACTGACGCTATGACGAAAGCGTGGGAGCAAAACAGATTAGATACCTGTGTAGTCCA 790
Db 749 TACTGACGCTATGACGAAAGCGTGGGAGCAAAACAGATTAGATACCTGTGTAGTCCA 690
Qy 791 CGCCCTAAACGATGCAACTAGTTGCTTGGGCTTACTAGGCTTGTGTAAGCTAAGCTAACGC 850
Db 689 CGCCCTAAACGATGCAACTAGTTGCTTGGGANTTTATTTCTTCAAGTAAAGCTAACGC 630
Qy 851 GTGAAGTTGACCGCTGGGAGTACGCTCGCAGGATTAATACTCAAAGGAAATTCACGGGG 910
Db 629 GTGAAGTTGACCGCTGGGAGTACGCTCGCAGGATTAATACTCAAAGGAAATTCACGGGG 570
Qy 911 ACCGCGACAAGCGGTGGATTTATGTGATTAATTCGATGCAACCGGAAATACTTACCTAC 970
Db 569 ACCGCGACAAGCGGTGGATTTATGTGATTAATTCGATGCAACCGGAAATACTTACCTAC 510
Qy 971 CTTTGACATGTAGCGAATTTTATAGATATAAATAGTGCCTTC--GGGAACTGCTAACACA 1028
Db 509 CTTTGACATGTAGCGAATTTTATAGATATAAATAGTGCCTTC--GGGAACTGCTAACACA 450
Qy 1029 GGTGTCATGGCTGCTCGTCAAGCTCGTGTGAGATGTTGGGTTAAAGTCCCGAACGAG 1088
Db 449 GGTGTCATGGCTGCTCGTCAAGCTCGTGTGAGATGTTGGGTTAAAGTCCCGAACGAG 390
Qy 1089 CGCAACCTTGTCAATTAATGCAATCATTTAGTTGGGCACCTTTAATGAGACTGCGCGTGA 1148
Db 389 CGCAACCTTGTCAATGCTGTACGAAA-----GGGCACTCTGATGGGACTGCGCGTGA 335
Qy 1149 CAACCGGAGAGGTGGGATGAGCTCAAGTCTCTCATGCGCCTTATGGGTAGGGCTTCA 1208
Db 334 CAACCGGAGAGGTGGGATGAGCTCAAGTCTCTCATGCGCCTTATAGGTGGGECTACA 275
Qy 1209 CACGTAATACAAATGGCGGTACAGAGGTGTCGAACCGCGAGGGGAGCTTAATCTCAGA 1268
Db 274 CACGTCATACAAATGGCGGTACAAAGGSCAGGAAAGCCGAGGTGAAGCCANTCCCAT 215
Qy 1269 AAGCGCGTGTAGTCGGATCGGAGTCTGCAACTCGACTCCGCTGGAAGTCCGGAATCGCTAG 1328
Db 214 AAGCGCGTGTAGTCGGATCGGAGTCTGCAACTCGACTCGCTGGAAGTCCGGAATCGCTAG 155
Qy 1329 TAATCGGGATCAGATGTCCGGTGAATAGCTTCCCGGGTCTTGTACACACCGCCGTC 1388
Db 154 TAATCGGGATCAGATGTCCGGTGAATAGCTTCCCGGGTCTTGTACACACCGCCGTC 95
Qy 1389 ACACATGGGAGTGGGTTTACCAGAACGATAGTCTTAACCGTAA--GAGGGCGTTTGCC 1447
Db 94 ACACATGGGAGTGGGTTTACCAGAACGATAGTCTTAACCGGAGGAGGGGCGCTTGCC 35
Qy 1448 ACGCGAGATTCATGACTGG 1467
Db 34 ACGGTGGGTTTCGTGACTGG 15
```

RESULT 13

US-09-735-567-6/c

; Sequence 6, Application US/09735567

; Patent No. 6608190

```
; GENERAL INFORMATION:
; APPLICANT: Bramucci, Michael
; TITLE OF INVENTION: Nucleic Acid Fragments for the Identification of Bacteria in
; TITLE OF INVENTION: Industrial Wastewater Bioreactors
; FILE REFERENCE: BC1033 US NA
; CURRENT APPLICATION NUMBER: US/09/735.567
; CURRENT FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/171,140
; PRIOR FILING DATE: 16 DECEMBER 1999
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 6
; LENGTH: 1539
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Brachyomonas
; OTHER INFORMATION: Nucleotide sequence of 16S rDNA corresponding to strain RA6
US-09-735-567-6
```

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Query Match 71.5%; Score 1048.4; DB 3; Length 1539;
Best Local Similarity 85.3%; Pred. No. 0;
Matches 1242; Conservative 0; Mismatches 201; Indels 13; Gaps 6;
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```
Qy 18 TGAACGCTGCGCGCATGCTTTACACATGCAAGTCGAACGCGCAGCACGGGTGCTTGCACCT 77
Db 1538 TGAACGCTGCGCGCATGCTTTACACATGCAAGTCGAACGCGCAGCGC--GTCTTCGGAT 1481
Qy 78 GGTGCGAGTGGCGGAGTGAATGATCGGAAGCTGTCCAGAAAGTGGGGGATTAAC 137
Db 1480 GCGCGGAGTGGCGAAGCGGTGAGTAAAGCATCGGAACGTCGCCGTAGTGGGATAGC 1421
Qy 138 GCATCGAAGATGTCTTAATACCGCATATCTCTACGAGGAGAAAGCAGGGGATC--GAAA 195
Db 1420 TCGCGAAGACCGGATTAATACCGCATGAGATCCGTGGATGAAAGCAGGACCGCGAAG 1361
Qy 196 GACCTTGTGCTTTTGGAGCGCCGATGCTGATTAGCTAGTTGGTGGGGTAAAGCCCTAC 255
Db 1360 GGCCTTGGCTACTTGGAGCGGCCGATGTCAGATTTAGGTAGTTGGTGGGGTAAAGCCAC 1301
Qy 256 CAAGGCAACGATCATGATGTTGTTCTGAGAGGACGACGACGACACTGGGACTGAGACAG 315
Db 1300 CAAGCTTGCATCTGTAGTGGTCTGAGAGGATGATCAGCCACATCGGGAATGAGACAG 1241
Qy 316 GCCCAGACTCTACGCGAGCGCAGTGGGAAATTTTGGCAATGGGCGAAGCCGCTGATC 375
Db 1240 GCCGAACTCTACGCGAGGCGAGTGGGAAATTTTGGCAATGGGCGAAGCCGCTGATC 1181
Qy 376 CAGCAATGCGCGGTGAGTGAAGAAGG--CTTCGGGTGTGTAAGCTCTTTTCACTCGAGAAGA 434
Db 1180 CAGCAATGCGCGGTGAGTGAAGAAGG--CTTCGGGTGTGTAAGCTCTTTTCACTCGAGAAGA 1121
Qy 435 AAAGGTTGTGACTAATTAATCAAACTTATGATGTACCGACAGAAAGACGACCGGCTAAC 494
Db 1120 AAAGGCTCTTTCTAATAAAGAGGCGCATGACGGTACCGTAAGAATAAGACACCGGCTAAC 1061
Qy 495 TACGTGCGCAGCAGCGCGTAAATACGTAGGTCGAAAGGTTAATCGGAATTAATCTGGGGT 554
Db 1060 TACGTGCGCAGCAGCGCGTAAATACGTAGGTCGAAAGGTTAATCGGAATTAATCTGGGGT 1001
Qy 555 AAAGGTTGTGACTAATTAATCAAACTTATGATGTGAAATCCCGGGCTTAACCTGGGAAT 614
Db 1000 AAAGGTTGTGACTAATTAATCAAACTTATGATGTGAAATCCCGGGCTTAACCTGGGAAT 941
Qy 615 TGCCTTTGAAACTAATAAGCTAGATGTACAGAGGGGGTGGAAATTCCTATGTGTAGCAG 674
Db 940 TGCCTTTGTGACTGCAAGGCTGGAGTACGCGCAGAGGGGATGGAATTCCTGCTGTAGCAG 881
Qy 675 TGAATCGGTAGATATGGAAGAACATCGATGCGGAGGCGCCCTCTGGGTTAACTACT 734
Db 880 TGAATCGGTAGATATGGAAGAACATCGATGCGGAGGCGCCCTCTGGGTTAACTACT 821
Qy 735 GACGCTCATGCAAGAAAGCGTGGGAGCAACAGGATTTAGATACCTCTGGTAGTCCACGCC 794
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Db      820  GACGCTCATGCGAAGACGTTGGGAGCAACACAGATTAGATACCCCTGGTAGTCCAGCC 761
Qy      795  CTAACAGATGCAACTAGTTGTTGGGCTTACTAGGCTTGGTAACTAGTAGTAAACGCGTGA 854
Db      760  CTAACAGATGCAACTAGTTGTTGGGATTTATTTCTTCAGTAAACGAGCTAACGCGTGA 701
Qy      855  AGTTGACCGCTGGGGAGTACGGTGCAGAGATTAAACTCAAGGAATTGACGGGAGCC 914
Db      700  AGTTGACCGCTGGGGAGTACGGCGCAAGGTTAAACTCAAGGAATTGACGGGAGCC 641
Qy      915  GCACAAGCGGTGGATTATGTGGATTAAATTCGATGCAACGCGCAAAACCTTACCTACCTT 974
Db      640  GCACAAGCGGTGGATTATGTGGTTTAAATTCGATGCAACGCGCAAAACCTTACCCACCTTT 581
Qy      975  GACATGTAGCGAATATTTTATAGAGATAAAATAGTCCCTTC--GGGACGCTAACACAGGTG 1032
Db      580  GACATGTATGGAATCCCGCAGAGATGTGGAGTGCTCGCAAGAGAGCCATAACACAGGTG 521
Qy      1033  CTGCATGGCTGCTGCAGCTGCTGCTGAGATGTTGGGTTAACTCCGCGCAACGAGCGCA 1092
Db      520  CTGCATGGCTGCTGCAGCTGCTGCTGAGATGTTGGGTTAACTCCGCGCAACGAGCGCA 461
Qy      1093  ACCCTTGTCAATTAATGTCATCAATTTAGTTGGGCACTTTAATGAGACTGCCGGTGACAAA 1152
Db      460  ACCCTTGGCATCAGTTGCTACGAAA-----GGGCACCTCTGATGGGACTGCCGGTGACAAA 406
Qy      1153  CCGAGAGAAAGTGGGGATGACGTCGTCATGCTCAAGTCCCTCATGGCCCTTATAGTGGGGCTACACAG 1212
Db      405  CCGAGAGAAAGTGGGGATGACGTCGTCATGCTCAAGTCCCTCATGGCCCTTATAGTGGGGCTACACAG 346
Qy      1213  TAATACAAATGGCGGTACAGAGGGTTGGCAACCCGCGAGGGGAGCTTAATCTCAGAAAGC 1272
Db      345  TCATACAAATGGCGGTACAAAGGGCAGCGAAGCCGCGAGGTGAAGCCCAATCCCAATAAAGC 286
Qy      1273  GCGTGTAGTCCGGATCGGAGTCTGCAACTCGACTCGTGAAGTCGGAATCGCTAGTAAT 1332
Db      285  CCGTGTAGTCCGGATCGGAGTCTGCAACTCGACTCGTGAAGTCGGAATCGCTAGTAAT 226
Qy      1333  GCGGATCAGCATGTCGGGTGAATACGTTCCCGGCTTTGTACACACCGCCGCTCACAC 1392
Db      225  CGTGATCAGCATGTCAGGTTGAATACGTTCCCGGCTTTGTACACACCGCCGCTCACAC 166
Qy      1393  CATGGGATGGGTTTCCAGGACAGATAGTCTAAACGTTAA--GAGGGCGTTTCCACGG 1451
Db      165  CATGGGATGGGTTTCCAGGACAGATAGTCTAAACGTTAA--GAGGGCGTTTCCACGG 106
Qy      1452  CGAGATTTCATGACTGG 1467
Db      105  TGGGGTTTCGTGACTGG 90

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RESULT 14
US-09-735-567-7
; Sequence 7, Application US/09735567
; Patent No. 6608190
; GENERAL INFORMATION:
; APPLICANT: Bramucci, Michael
; TITLE OF INVENTION: Nucleic Acid Fragments for the Identification of Bacteria in
; TITLE OF INVENTION: Industrial Wastewater Bioreactors
; FILE REFERENCE: BC1033 US NA
; CURRENT APPLICATION NUMBER: US/09/735,567
; CURRENT FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/171,140
; PRIOR FILING DATE: 16 DECEMBER 1999
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 7
; LENGTH: 1454
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Brachyomonas

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; OTHER INFORMATION: Nucleotide sequence of the 16S rDNA corresponding to strain RA9
US-09-735-567-7
Query Match 71.4%; Score 1047.8; DB 3; Length 1454;
Best Local Similarity 85.2%; Pred. No. 0;
Matches 1242; Conservative 0; Mismatches 202; Indels 13; Gaps 6;

Qy      17  TTGAACGCTGGCGCATGCTTTACACATGCAAGTTCGAAAGCGGACGCGGTGCTTGCAACC 76
Db      1  TTGAACGCTGGCGCATGCTTTACACATGCAAGTTCGAAAGCGGACGCGC--GTCTCTCGGGA 58
Qy      77  TGTGGCGAGTGGCGGACGGTGTAGTAATCATCTCGAAACGCTGTCCAGAAAGTGGGGGATAA 136
Db      59  TGGCGGCGAGTGGCGGACGGTGTAGTAATCATCTCGAAACGCTGTCCCGGTAGTGGGGGATAG 118
Qy      137  CGCATCGAAAGATGTGTCTAATACCGCATATTTCTCTACGAGGAAAGCAGGGGA--TCGAA 194
Db      119  CTGGCGGAAAGCGGATTTAATACCGCATGAGATCCGTTGGATGAAAGCAGGGGACTCGCAA 178
Qy      195  AGACCTTGTGCTTTTGGAGCGCGCGATGCTCTGATTTAGTCTAGTTGGTGGGTAAAGGCTTA 254
Db      179  GGGCCCTTGGCGCTACTTGGAGCGCGCGATGTCAGATTTAGTGTGGTGGGTAAAGGCGCCA 238
Qy      255  CCAAGGCAACGATCAGTAGTTGTCTGAGAGGACGACACGACACATCTGGGACTGAGACAC 314
Db      239  CCAAGGCTGCGATCTGTAGTCTGTCTGAGAGGATGATCAGCCACATCGGAGCTGAGACAC 298
Qy      315  GGCCCAAGACTCTTACGGGAGGCGAGTAGTGGGGAATTTTGGCAATGTTGGCGAAAGCCTGAT 374
Db      299  GGCCCGCAACTCTTACGGGAGGCGAGTAGTGGGGAATTTTGGCAATGTTGGCGCAAGCCTGAT 358
Qy      375  CAGCAATGCGCGCTGAGTGAAGAAAG--CTTCCGGTTGTAAAGCTCTTTTCAGTTCGAGAAG 433
Db      359  CCAAGCCTATGCGCGTGCAGATGAAGGCTTCCGGTTGTAAAGCTCTTTTCAGTTCGAGAAG 418
Qy      434  AAAAGGTTGTGATTAATAATCAAACTTATGATGTGTACCGACAGAAAGACGACCGGCTAA 493
Db      419  AAAGGCTCTTTCTAATTAAGAGGGACATGACGGTACCGTAAAGATTAAGACGCGGCTAA 478
Qy      494  CTACGTGCCAGCAGCGCGCTTAATACTAGGGTGAAGCGCTTAATCGGAATTAATCTGGGCG 553
Db      479  CTACGTGCCAGCAGCGCGCTTAATACTAGGGTGAAGCGCTTAATCGGAATTAATCTGGGCG 538
Qy      554  TAAAGGTTGCGCAGCGCGCTTTGTAGTCAAGTGTGAAATCCCGGCTTAACTCGGAA 613
Db      539  TAAAGGTTGCGCAGCGCGCTTTGTAGTCAAGTGTGAAATCCCGGCTTAACTCGGAA 598
Qy      614  TTGCGTTTGAACCTACAAAGCTAGAGTGTAGCAGAGGGGGGTGGAATTCATGTGTAGCA 673
Db      599  CTGCCATTGTGACTGCAAGGCTGAGTACGGCAGAGGGGGATGGNATTCGCGGTGTAGCA 658
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Qy      734  TGAGCTCATGCAAGAAAGCGTGGGAGCAACAGGATTTAGATACCTGCTAGTCCACGC 793
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RESULT 15

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US-09-228-184-1
; Sequence 1, Application US/09228184
; Patent No. 6322782
; GENERAL INFORMATION:
; APPLICANT: WALKER, Harrell L.
; TITLE OF INVENTION: CONTROL OF CYANOBACTERIA WITH A BACTERIUM
; FILE REFERENCE: 013243-0007
; CURRENT APPLICATION NUMBER: US/09/228,184
; CURRENT FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1540
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Bacterium SG-3;
; OTHER INFORMATION: gram negative; rod-shaped; exhibits flagellate
; OTHER INFORMATION: motility; pathogenic to cyanobacteria and algae;
; OTHER INFORMATION: yellow colonies on BG-11 medium suppl. with tryptic
US-09-228-184-1

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Query Match 70.7%; Score 1037.6; DB 3; Length 1540;
Best Local Similarity 84.1%; Pred. No. 0;
Matches 1243; Conservative 0; Mismatches 224; Indels 11; Gaps 6;

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Job time : 304 secs


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DEFINITION Sequence 20 from Patent WO2004026772.
ACCESSION CQ796927
VERSION CQ796927.1 GI:46408553
KEYWORDS .
SOURCE unidentified
ORGANISM unidentified
REFERENCE unclassified sequences.
1 Hovanec, T. A.
AUTHORS Ammonia-oxidizing bacteria and methods of using and detecting
TITLE thesame
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Aquaaria Inc. (US)
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Best Local Similarity 99.7%; Pred. No. 7.9e-18;
Matches 1464; Conservative 0; Mismatches 3; Indels 2; Gaps 2;
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DEFINITION AF272420
ACCESSION AF272420.1 GI:11545280
VERSION
KEYWORDS
SOURCE Nitrosomonas aestuarii
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ORGANISM Nitrosomonas aestuarii
Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
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REFERENCE 1 (bases 1 to 1450)
AUTHORS Purkhold, U., Pommerening-Rosser, A., Juretschko, S., Schmid, M.C.,
Koops, H.P. and Wagner, M.
TITLE Phylogeny of all recognized species of ammonia oxidizers based on
comparative 16S rRNA and amoA sequence analysis: implications for
molecular diversity surveys
JOURNAL Appl. Environ. Microbiol. 66 (12), 5368-5382 (2000)
PUBMED 11097916
REFERENCE 2 (bases 1 to 1450)
AUTHORS Purkhold, U., Pommerening-Rosser, A., Juretschko, S., Schmid, M.C.,
Koops, H.P. and Wagner, M.
TITLE Direct Submission
JOURNAL Submitted (26-MAY-2000) Lehrstuhl fuer Mikrobiologie, Technische
Universitaet Muenchen, Am Hochanger 4, Freising 85350, Germany
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Best Local Similarity 99.7%; Pred. No. 1,7e-17;
Matches 1445; Conservative 0; Mismatches 3; Indels 2; Gaps 2;
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QY 1455 GATTTCATGAC 1464
Db 1441 GATTTCATGAC 1450

RESULT 5
LOCUS CQ796926 1494 bp DNA linear PAT 19-APR-2004
DEFINITION Sequence 19 from Patent WO2004026772.
ACCESSION CQ796926
VERSION CQ796926.1 GI:46408552

KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified sequences.

REFERENCE
1
AUTHORS Hovanec, T. A.
TITLE Ammonia-oxidizing bacteria and methods of using and detecting
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JOURNAL Patent: WO 2004026772-A 19 01-APR-2004;

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Best Local Similarity 98.1%; Pred. No. 3.4e-17;
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 DEFINITION AF272424
 ACCESSION AF272424
 VERSION AF272424.1 GI:11545284
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 SOURCE Nitrosomonas sp. Nm51
 ORGANISM Nitrosomonas sp. Nm51
 Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
 Nitrosomonadaceae; Nitrosomonas.
 REFERENCE 1 (bases 1 to 1513)
 AUTHORS Purkhold,U., Pommerening-Roser,A., Juretschko,S., Schmid,M.C.,
 Koops,H.P. and Wagner,M.
 TITLE Phylogeny of all recognized species of ammonia oxidizers based on
 comparative 16S rRNA and amoA sequence analysis: implications for
 molecular diversity surveys
 JOURNAL Appl. Environ. Microbiol. 66 (12), 5368-5382 (2000)
 PUBMED 11097916
 REFERENCE 2 (bases 1 to 1513)
 AUTHORS Purkhold,U., Pommerening-Roser,A., Juretschko,S., Schmid,M.C.,
 Koops,H.P. and Wagner,M.
 TITLE Direct Submission
 JOURNAL Submitted (26-MAY-2000) Lehrstuhl fuer Mikrobiologie, Technische
 Universitaet Muenchen, Am Hochanger 4, Freising 85350, Germany
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 rRNA

ORIGIN
 Query Match 94.6%; Score 1388.2; DB 1; Length 1513;
 Best Local Similarity 97.5%; Pred. No. 6.1e-17;
 Matches 1430; Conservative 0; Mismatches 34; Indels 2; Gaps 2;
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RESULT 7
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 DEFINITION AF272418
 ACCESSION AF272418.1 GI:11545278
 VERSION
 KEYWORDS
 SOURCE Nitrosomonas marina
 ORGANISM Nitrosomonas marina
 Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
 Nitrosomonadaceae; Nitrosomonas.
 REFERENCE 1 (bases 1 to 1492)
 AUTHORS Purkhold,U., Pommerening-Roser,A., Juretschko,S., Schmid,M.C.,
 Koops,H.P. and Wagner,M.
 TITLE Phylogeny of all recognized species of ammonia oxidizers based on
 comparative 16S rRNA and amoA sequence analysis: implications for
 molecular diversity surveys
 JOURNAL Appl. Environ. Microbiol. 66 (12), 5368-5382 (2000)
 PUBMED 11097916
 REFERENCE 2 (bases 1 to 1492)
 AUTHORS Purkhold,U., Pommerening-Roser,A., Juretschko,S., Schmid,M.C.,
 Koops,H.P. and Wagner,M.
 TITLE Direct Submission
 JOURNAL Submitted (26-MAY-2000) Lehrstuhl fuer Mikrobiologie, Technische
 Universitaet Muenchen, Am Hochanger 4, Preisang 85350, Germany
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RESULT 8
AF386752 1457 bp DNA linear ENV 10-MAY-2004
LOCUS Nitrosomonas sp. R7c131 16S ribosomal RNA gene, partial sequence.
DEFINITION AF386752
ACCESSION AF386752.1 GI:17864829
VERSION ENV.
KEYWORDS Nitrosomonas sp. R7c131
SOURCE Nitrosomonas sp. R7c131
ORGANISM Nitrosomonas sp. R7c131
Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
Nitrosomonadaceae; Nitrosomonas; environmental samples.
REFERENCE 1 (bases 1 to 1457)
AUTHORS Burrell,P.C., Phalen,C.M. and Hovanec,T.A.
TITLE Identification of bacteria responsible for ammonia oxidation in
freshwater aquaria
JOURNAL Appl. Environ. Microbiol. 67 (12), 5791-5800 (2001)
PUBMED 11722936
REFERENCE 2 (bases 1 to 1457)
AUTHORS Burrell,P.C., Phalen,C.M. and Hovanec,T.A.
TITLE Direct Submission
JOURNAL Submitted (30-MAY-2001) Aquatic Research Laboratory, The Aquaria
Group, 6100 Condon Dr, Moorpark, CA 93021, USA
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Db 601 TGCCTTTGAAACTACAAAGCTAGAGTGTACAGAGGGGGGTGGAATTCATGTGTAGCAG 660
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DEFINITION Sequence 1 from Patent WO2004026772.
ACCESSION CQ796908
VERSION CQ796908.1 GI:46408534
KEYWORDS .
SOURCE unidentified
ORGANISM unidentified
unclassified sequences.
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REFERENCE
AUTHORS Hovanec,T.A.
TITLE Ammonia-oxidizing bacteria and methods of using and detecting
thesame
JOURNAL Patent: WO 2004026772-A 1 01-APR-2004;
Aquaaria Inc. (US)
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Best Local Similarity 97.2%; Pred. No. 2e-16;
Matches 1414; Conservative 0; Mismatches 3; Indels 3; Gaps 3;
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LOCUS CS089154 1457 bp DNA linear PAT 25-MAY-2005
 DEFINITION Sequence 1 from Patent EP1502948.
 ACCESSION CS089154
 VERSION CS089154.1 GI:66714438
 KEYWORDS unidentified
 SOURCE unclassified
 ORGANISM unclassified
 REFERENCE 1
 AUTHORS Hovanec, T.A. and Burrell, P.C.
 TITLE Ammonia-oxidizing Bacteria
 JOURNAL Patent: EP 1502948-A 1 02-FEB-2005;
 Aquaria Inc. (US)
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 Best Local Similarity 97.2%; Pred. No. 2e-16;
 Matches 1414; Conservative 0; Mismatches 37; Indels 3; Gaps 3;
 QY 16 ATTGAACGCTGGCGCATGCTTTACACATGCAAGTCGAACGGCAGCAGCGGTGCTTGAC 75
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 DB 241 CAAGGCGAGATCAGTAGTTGCTGAGAGGACGACAGCAGCAGCTGGGACTGAGACACG 300
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 DEFINITION Sequence 2 from Patent EP1502948.
 ACCESSION CS089155
 VERSION CS089155.1 GI:66714439
 KEYWORDS
 SOURCE unidentified
 ORGANISM unclassified
 REFERENCE 1
 AUTHORS Hovanec, T.A. and Burrell, P.C.
 TITLE Ammonia-oxidizing Bacteria
 JOURNAL Patent: EP 1502948-A 2 02-FEB-2005;
 Aquaria Inc. (US)
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VERSION	AX316092.1	GI:17899283				
KEYWORDS	.	unidentified				
SOURCE		unidentified				
ORGANISM		unclassified sequences.				
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AUTHORS	Hovanec, T.A. and Burrell, P.C.					
TITLE	Ammonia-oxidizing bacteria					
JOURNAL	Patent: WO 0190312-A 1 29-NOV-2001;					
	AQUARIA, INC. (US)					
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Qy	76	CTGGTGGCGAGTGGCGGACGCGGTGAGTAATGCAATCGGAACGTGTCCAGAAAGTGGGGGATA	135						
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Db 961 GACATGTAGCGAAATATTTTAGAGTAAATAATAGTGCCTTCGGGAACGCTTAACACAGGTGCT 1019
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QY 1095 CTTTGTCAATTAATGCCATCACTTTAGTTGGGCACTTTTAATGAGACTGCCGTGACAAACC 1154
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QY 1155 GGAGAAGGTGGGATGACGTCAAAGTCTCATGCGCCCTTATGGGTAGGGCTTCAACGTA 1214
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QY 1215 ATCAATGGCCGCTACAGAGGGTTGCCAACCCGAGGGGAGCTAATCTCAGAAAGGCG 1274
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Db 1260 GTCGTAGTCCGGATCGGAGTCTGCAACTCGACTCCGTGAAGTCCGGAATCGCTAGTAATCG 1319
QY 1335 CGGATCAGCATGTCCGGTGAATACGTTCCGGTCTTGTATACACACCGCCGTCACACCA 1394
Db 1320 CGGATCAGCATGTCCGGTGAATACGTTCCGGTCTTGTATACACACCGCCGTCACACCA 1379
QY 1395 TGGAGTGGGTTTCCACAGACGAGTAGTCTTAACCGTAA-GAGGGGTTGGCCACCGCG 1453
Db 1380 TGGAGTGGGTTTCCACAGACGAGTAGTCTTAACCGTAA-GAGGGGTTGGCCACCGCG 1439
QY 1454 AGATTCATGACTGG 1467
|||||

Db 1440 AGATTCATGACTGG 1453
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AF386757
LOCUS 1457 bp DNA linear ENV 10-MAY-2004
DEFINITION Nitrosomonas sp. R7c187 16S ribosomal RNA gene, partial sequence.
ACCESSION AF386757
VERSION AF386757.1 GI:17864834
KEYWORDS ENV.
SOURCE Nitrosomonas sp. R7c187
ORGANISM Nitrosomonas sp. R7c187
Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
Nitrosomonadaceae; Nitrosomonas; environmental samples.
REFERENCE 1 (bases 1 to 1457)
AUTHORS Burrell,P.C., Phalen,C.M. and Hovanec,T.A.
TITLE Identification of bacteria responsible for ammonia oxidation in freshwater aquaria
JOURNAL Appl. Environ. Microbiol. 67 (12), 5791-5800 (2001)
PUBMED 11722936
REFERENCE 2 (bases 1 to 1457)
AUTHORS Burrell,P.C., Phalen,C.M. and Hovanec,T.A.
TITLE Direct Submission
JOURNAL Submitted (30-MAY-2001) Aquatic Research Laboratory, The Aquaria Group, 6100 Condon Dr, Moorpark, CA 93021, USA
FEATURES
Location/Qualifiers
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/product="16S ribosomal RNA"
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Best Local Similarity 97.2%; Pred. No. 2.2e-16;
Matches 1413; Conservative 0; Mismatches 38; Indels 3; Gaps 3;
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Db 1 ATTGAACGCTGGCGGATGCTTTACATGCAAGTGAACGCGACGACGGTGTTCAT 60
QY 76 CTGGTCGAGTGC CGGACGCGGTGAGTAATGCATCGGAACGTGTCCAGAAAGTGGGGATA 135
Db 61 CTGGTCGAGTGC CGGACGCGGTGAGTAATGCATCGGAACGTATCCAGAAAGGGGGATA 120
QY 136 ACGCATCGAAGATGCTTAATACCGCATATTTCTACGAGGAGGAGGAGGATCGAAA 195
Db 121 ACGCATCGAAGATGCTTAATACCGCATATTTCTAAGGAGGAGGAGGATCGAAA 180
QY 196 GACCTTGTGCTTTTGAGCGCGCGATGCCTGATAGCTAGTTGGTGGGTAAAGGCTAC 255
Db 181 GACCTTGGCTTTTGAGCGCGCGATGCTGATAGCTAGTTGGTGGGTAAAGGCTAC 240
QY 256 CAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACAGCCACTGGGACTGAGACAG 315
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Db 301 GCCCAGACTCTACGGAGGCGCAGTGGGGAATTTTGGACAATGGCGCAAGCCTGATC 360
QY 376 CAGCAATGCCGCTGAGTGAAGAAGG-CTTCGGGTTGTAAAGCTCTTTCAAGTCGAGAAGA 434
Db 361 CAGCAATGCCGCTGAGTGAAGAAGGCTTCGGGTTGTAAAGCTCTTTCAAGTCGAGAAGA 420
QY 435 AAAGGTTGTGACTTAATAATCAAACTTATGATGTGTACCGACAGAGAAGACCGGCTAAC 494
Db 421 AAAGGTTTACGGTAAATAATCTGACTCATGACGGTATCGACAGAAGAAGACCGGCTAAC 480

QY	495	TACGTGCCACGAGCCGCGTAAATACGTAGGTGCAAGCGTTAATCGGAATTACTGGCGT	554
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QY	555	AAAGGTCGCGAGGCGGCTTTCTAAGTCAAGTGTGAATCCCGGCTTTAACTGGGAAT	614
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QY	615	TGCGTTTGAACCTACAAAGCTAGAGTGTGGCAGAGGGGAGGTGGAATCCATGTGTAGCAG	674
Db	601	TGCGTTTGAACCTACAAAGCTAGAGTGTGGCAGAGGGGAGGTGGAATCCATGTGTAGCAG	660
QY	675	TGAAATGGCTAGAGATATCGAAGAACATCGATGGCGAAGCGAGCCCTGGGTTAACACT	734
Db	661	TGAAATGGCTAGAGATATCGAAGAACATCGATGGCGAAGCGAGCCCTGGGTTAACACT	720
QY	735	GACGCTCATGCAAGGCGTGGGAGCAAAACAGATTAGATACCCCTGGTGTAGTCCACGCC	794
Db	721	GACGCTCATGCAAGGCGTGGGAGCAAAACAGATTAGATACCCCTGGTGTAGTCCACGCC	780
QY	795	CTAAAGCATGTCAACTAGTGTGGGCCCTTACTAGGCTTGGTAAAGTGTAGCTAACCGGTGA	854
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QY	855	AGTTGACCGCTGGGAGTACGCTCGAGGATTTAAAGCTCAAGGAAATTTGACGGGGACCC	914
Db	841	AGTTGACCGCTGGGAGTACGCTCGAGGATTTAAAGCTCAAGGAAATTTGACGGGGACCC	900
QY	915	GCACAAGCGGTGGATTATGTGGATTAAATTCGATGCAACCGGAAACCTTACCTACCCCTT	974
Db	901	GCACAAGCGGTGGATTATGTGGATTAAATTCGATGCAACCGGAAACCTTACCTACCCCTT	960
QY	975	GACATGTAGCGAATATTTAGAGATAAATAGTGCCTTCGGGAACGCTAAACACAGGTGCT	1034
Db	961	GACATGTAGCGAATATTTAGAGATAAATAGTGCCTTCGGGAACGCTAAACACAGGTGCT	1019
QY	1035	GCATGGCTGTGCTGAGTGTGCTGAGATGTTGGGTTTAACTCCGCAACGAGCGCAAC	1094
Db	1020	GCATGGCTGTGCTGAGTGTGCTGAGATGTTGGGTTTAACTCCGCAACGAGCGCAAC	1079
QY	1095	CCTTGTCAATTAATGCCATCATTTAGTTGGGCACCTTTAATGAGACTGCCGGTGAACAAACC	1154
Db	1080	CCTTGTCAATTAATGCCATCATTTAGTTGGGCACCTTTAATGAGACTGCCGGTGAACAAACC	1139
QY	1155	GGAGGAAGTGGGATGAGTCAAGTCTCATGGCCCTTATGGGTAGGCTTTCAACGTA	1214
Db	1140	GGAGGAAGTGGGATGAGTCAAGTCTCATGGCCCTTATGGGTAGGCTTTCAACGTA	1199
QY	1215	ATACAATGGCGGTACAGGGGTTGCCAACCGCGAGGGGAGCTAATCTCAGAAAGCGC	1274
Db	1200	ATACAATGGCGGTACAGGGGTTGCCAACCGCGAGGGGAGCTAATCTCAGAAAGCGC	1259
QY	1275	GTCTAGTCCGGATCGGAGTCTGCAACTCGACTCCGTGAAGTCGGAATCGCTAGTAATCG	1334
Db	1260	GTCTAGTCCGGATCGGAGTCTGCAACTCGACTCCGTGAAGTCGGAATCGCTAGTAATCG	1319
QY	1335	CGGATCAGCATGTCCGGTGAATAAGTTCCTCCGGGTTGTATACACCGCCCGTCAACCA	1394
Db	1320	CGGATCAGCATGTCCGGTGAATAAGTTCCTCCGGGTTGTATACACCGCCCGTCAACCA	1379
QY	1395	TGGGAGTGGGTTTACCAGAACAGATAGTCTAACCGTAA-CAGGGCGTTTCCACGGCG	1453
Db	1380	TGGGAGTGGGTTTACCAGAACAGATAGTCTAACCGTAAAGGAGGCGCTTCCACGGGTG	1439
QY	1454	AGATTTCATGACTGG	1467
Db	1440	AGATTTCATGACTGG	1453

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 6, 2006, 19:12:36 ; Search time 936 Seconds
(without alignments)
10445.624 Million cell updates/sec

Title: US-10-659-983A-18

Perfect score: 1467

Sequence: 1 ttgatcatggctcagattga.....acggcgagattcatgactgg 1467

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: geneseqn1990s:*
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13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1467	100.0	1467	12	ADM32721 AOB P4c10
2	1440.2	98.2	1491	12	ADM32723 AOB BF16c
3	1403.4	95.7	1494	12	ADM32722 AOB P4c10
4	1358.8	92.6	1457	6	ABAO2416 Type A am
5	1358.8	92.6	1457	12	ADM32704 AOB Type
6	1357.2	92.5	1457	6	ABAO2417 Type A1 a
7	1357.2	92.5	1457	12	ADM32705 AOB Type
8	1252	85.3	1458	6	ABAO2418 Type B am
9	1252	85.3	1458	12	ADM32706 AOB Type
10	1210.6	82.5	1460	6	ABAO2419 Type C am
11	1210.6	82.5	1460	12	ADM32707 AOB Type
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13	1189	81.0	1485	4	AAC86030 16S rDNA,
14	1171.2	79.8	1460	4	AAC86026 16S rDNA,
15	1170.2	79.8	1530	13	ADR45500 16S rRNA
16	1162.8	79.3	1460	4	AAC86024 R.tenuis
17	1151.8	78.5	1459	4	AAC86028 16S rDNA,
18	1150.4	78.4	1464	6	ABL40355 Sequence
19	1145.2	78.1	1460	4	AAC86022 R. tenuis

20	1144.2	78.0	1460	4	AAC86021
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22	1141.2	77.8	1478	4	AAC86023
23	1132.2	77.2	1535	2	AAV24295
24	1132.2	77.2	1535	10	ADB61689
25	1131.8	77.2	1532	2	AAQ26729
26	1131.8	77.2	1532	10	ADB61686
27	1130.4	77.1	1426	4	AAC86029
28	1128.2	76.9	1530	14	ADM12666
29	1120.6	76.4	1532	2	AAQ64008
30	1116.8	76.1	1464	10	ADB61688
31	1113.2	75.9	1485	10	ADB61687
32	1110.2	75.7	1509	12	ADQ67895
33	1108.6	75.6	1509	12	ADQ67894
34	1106.2	75.4	1610	10	ADB61691
35	1104.2	75.3	1400	8	ABZ69298
36	1104	75.3	1536	2	AAT18765
37	1103.4	75.2	1452	6	ABV72366
38	1103.4	75.2	1496	12	ADQ16355
39	1103.4	75.2	1496	14	AEA01071
40	1102.2	75.2	1400	8	ABZ69299
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44	1101.6	75.1	110000	3	AAA81490_00
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ALIGNMENTS

RESULT 1
ADM32721
ID ADM32721 standard; DNA; 1467 BP.

XX
AC ADM32721;

XX
DT 17-JUN-2004 (first entry)

XX
DE AOB P4clone42 16S rDNA.

XX
KW 16S rDNA; ammonia oxidising bacteria; AOB; ammonia; nitrite;
XX
KW aqueous environment; freshwater; seawater; aquarium; ss.

XX
OS Nitrosomonas aestuarii.

XX
FN WO2004026772-A2.

XX
PD 01-APR-2004.

XX
PF 10-SEP-2003; 2003WO-US028210.

XX
PR 19-SEP-2002; 2002US-0386217P.

PR 19-SEP-2002; 2002US-0386218P.

PR 19-SEP-2002; 2002US-0386219P.

PA (AQUA-) AQUARIA INC.

PI Hovanec TA;

XX
DR WPI; 2004-304936/28.

PT New composition comprising an isolated bacterial strain that oxidizes
PT ammonia to nitrite, useful for alleviating or preventing the accumulation
PT of ammonia in aqueous environment.

XX
Claim 1; Page 13; 98pp; English.

CC This sequence represents a 16S rDNA sequence derived from an ammonia
CC oxidising bacteria (AOB). This sequence may be used in a composition
CC which comprises an isolated bacterial strain that oxidizes ammonia to
CC nitrite. The composition may be used for alleviating or preventing the
CC accumulation of ammonia in a medium. The ammonia is reduced by at least

CC 30% when compared with a level of ammonia that would exist in the absence
 CC of the bacterial strain. The composition is useful for alleviating or
 CC preventing the accumulation of ammonia in aqueous environment, e.g. a
 CC freshwater or seawater aquarium.

XX SQ Sequence 1467 BP; 384 A; 320 C; 451 G; 312 T; 0 U; 0 Other;

Query Match 100.0%; Score 1467; DB 12; Length 1467;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1467; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	TTGATCATGGCTCAGATTGAACGCTGGCGCATGCTTTTACACATGCAAGTCGAACGGCAG	60
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Qy	61	CACGGGTGCTTGCACTGGTGGCGAGTGGCGGACGGGTGAGTAAATGATCGGAACGTTGTC	120
Db	61	CACGGGTGCTTGCACTGGTGGCGAGTGGCGGACGGGTGAGTAAATGATCGGAACGTTGTC	120
Qy	121	CAGAAGTGGGGGTAAGCGATCGAAAGATGTCTTAATACCGCATATTTCTCTACGGAGGAA	180
Db	121	CAGAAGTGGGGGTAAGCGATCGAAAGATGTCTTAATACCGCATATTTCTCTACGGAGGAA	180
Qy	181	AGCAGGGGATCGAAGACCTTGTCTTTTGGAGCGCGGATGCTGATTAAGCTAGTTGGT	240
Db	181	AGCAGGGGATCGAAGACCTTGTCTTTTGGAGCGCGGATGCTGATTAAGCTAGTTGGT	240
Qy	241	GGGGTAAAGGCTTACCAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCGCCACAC	300
Db	241	GGGGTAAAGGCTTACCAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCGCCACAC	300
Qy	301	TGGGACTGAGACACGGCCAGACTCTTACGGGAGGACGAGTGGGGAATTTTGGACAATG	360
Db	301	TGGGACTGAGACACGGCCAGACTCTTACGGGAGGACGAGTGGGGAATTTTGGACAATG	360
Qy	361	GGCGAAGCCTGATCCAGCATCGCGGTGATGCAAGAGCTTTCGGTGTGTAAGCTCT	420
Db	361	GGCGAAGCCTGATCCAGCATCGCGGTGATGCAAGAGCTTTCGGTGTGTAAGCTCT	420
Qy	421	TTCACTCGAGAGAAAGGTTGTGACTAATAATCACAACTTATGATGGTACCGACAGAAG	480
Db	421	TTCACTCGAGAGAAAGGTTGTGACTAATAATCACAACTTATGATGGTACCGACAGAAG	480
Qy	481	AAGCACCGGCTAATACGTGCGCAGCAGCGCGGTAAATACGTAGGGTGCNAGCGTTATCG	540
Db	481	AAGCACCGGCTAATACGTGCGCAGCAGCGCGGTAAATACGTAGGGTGCNAGCGTTATCG	540
Qy	541	GAATTTACTGGGCTAAAGGGTGGCGAGCGGCTTTTGAAGTCAGATGTGAAATCCCGGG	600
Db	541	GAATTTACTGGGCTAAAGGGTGGCGAGCGGCTTTTGAAGTCAGATGTGAAATCCCGGG	600
Qy	601	CTTAACTGGGAAATTCGTTTGAACCTAACAAGCTAGAGTGTACAGAGGGGGTGGAAAT	660
Db	601	CTTAACTGGGAAATTCGTTTGAACCTAACAAGCTAGAGTGTACAGAGGGGGTGGAAAT	660
Qy	661	TCCATGTGTACAGTGAATTCGTAGATATGGAAGAACATCGATGGCGAAGCGAGCCC	720
Db	661	TCCATGTGTACAGTGAATTCGTAGATATGGAAGAACATCGATGGCGAAGCGAGCCC	720
Qy	721	CCTGGGTTAACTGACGCTCATGCAAGAAAGCGTGGGGAGCAAAACAGGATTAGATACCC	780
Db	721	CCTGGGTTAACTGACGCTCATGCAAGAAAGCGTGGGGAGCAAAACAGGATTAGATACCC	780
Qy	781	TGGTAGTCCACCGCCCTAAACGATGTCAACTAGTTGTTGGGCTTACTAGGCTTGGTAACG	840
Db	781	TGGTAGTCCACCGCCCTAAACGATGTCAACTAGTTGTTGGGCTTACTAGGCTTGGTAACG	840
Qy	841	TAGCTAACCGCTGAGTTTGAACGCTGGGAGTACGGTCGAGGATTAABACTCAAAGGA	900
Db	841	TAGCTAACCGCTGAGTTTGAACGCTGGGAGTACGGTCGAGGATTAABACTCAAAGGA	900
Qy	901	ATTGACGGGGACCCGCAACAGCGGTGGATTATGTGGATTAAATTCGATGCAACGCGGAAAA	960

Db	901	ATTGACGGGGACCCGCAACGCGGTGGATTATGTGGATTAAATTCGATGCAACGCGAAAAA	960
Qy	961	CCTTACCTACCTTGACATGTAGCGAATATTTTAGAGATAAAATAGTGCCTTCGGGAACG	1020
Db	961	CCTTACCTACCTTGACATGTAGCGAATATTTTAGAGATAAAATAGTGCCTTCGGGAACG	1020
Qy	1021	CTAAACACAGTGTGCTGATGCTGCTGAGCTCGTGTGCTGAGATGCTGGGTTAAGTCCC	1080
Db	1021	CTAAACACAGTGTGCTGATGCTGCTGAGCTCGTGTGCTGAGATGCTGGGTTAAGTCCC	1080
Qy	1081	GCAACGAGCGCAACCCCTTCTCATTAATTCGCCATCATTTAGTTGGGCATTTAATGAGACT	1140
Db	1081	GCAACGAGCGCAACCCCTTCTCATTAATTCGCCATCATTTAGTTGGGCATTTAATGAGACT	1140
Qy	1141	GCGGTGACAAACCGGAGGAGGTGGGGATGAGTCAAGTCCCTCATGCGCCCTTATGGGTA	1200
Db	1141	GCGGTGACAAACCGGAGGAGGTGGGGATGAGTCAAGTCCCTCATGCGCCCTTATGGGTA	1200
Qy	1201	GGGCTTCAACAGCTAATACAAATGGCGGTACAGAGGTTGCCAAACCGCGAGGGGAGCTA	1260
Db	1201	GGGCTTCAACAGCTAATACAAATGGCGGTACAGAGGTTGCCAAACCGCGAGGGGAGCTA	1260
Qy	1261	ATCTCAGAAAGCGCGTCTGATGTCGGATCGGATCTGCAACTCGACTCCGTGAAGTCGGA	1320
Db	1261	ATCTCAGAAAGCGCGTCTGATGTCGGATCGGATCTGCAACTCGACTCCGTGAAGTCGGA	1320
Qy	1321	ATCGCTAGTAATTCGGGATCAGCATGTCCGGGTGANTAGTTCGGGGTCTTGTACACAC	1380
Db	1321	ATCGCTAGTAATTCGGGATCAGCATGTCCGGGTGANTAGTTCGGGGTCTTGTACACAC	1380
Qy	1381	CGCGCTCAGACCATGGGAGTGGGTTTCCACAGAACAGATAGTCTTAAACCGTAAGAGGGC	1440
Db	1381	CGCGCTCAGACCATGGGAGTGGGTTTCCACAGAACAGATAGTCTTAAACCGTAAGAGGGC	1440
Qy	1441	GTTTGGCACGGCGAGATTTCATGACTGG	1467
Db	1441	GTTTGGCACGGCGAGATTTCATGACTGG	1467

RESULT 2
 ADM32723
 ID ADM32723 standard; DNA; 1491 BP.

AC	ADM32723;
XX	
XX	17-JUN-2004 (first entry)
DT	
XX	AOB BF16clone57 16S rDNA.
XX	
XX	16S rDNA; ammonia oxidising bacteria; AOB; ammonia; nitrite;
KW	aqueous environment; freshwater; seawater; aquarium; ss.
XX	
OS	Nitrosomonas aestuarii.
XX	
PN	WO2004026772-A2.
XX	
PD	01-APR-2004.
XX	
PF	10-SEP-2003; 2003WO-US028210.
XX	
PR	19-SEP-2002; 2002US-0386217P.
XX	
PR	19-SEP-2002; 2002US-0386218P.
XX	
PR	19-SEP-2002; 2002US-0386219P.
XX	
PA	(AQUA-) AQUARIA INC.
XX	
PI	Hovanec TA;
XX	
PI	WPI; 2004-304936/28.
XX	
DR	
XX	
PT	New composition comprising an isolated bacterial strain that oxidizes
PT	ammonia to nitrite, useful for alleviating or preventing the accumulation
PT	of ammonia in aqueous environment.

XX
PS
XX
CC
CC
CC
CC
CC
CC
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SQ

Claim 1; Page 15; 98pp; English.

This sequence represents a 16S rDNA sequence derived from an ammonia oxidising bacteria (AOB). This sequence may be used in a composition to which comprises an isolated bacterial strain that oxidizes ammonia to nitrite. The composition may be used for alleviating or preventing the accumulation of ammonia in a medium. The ammonia is reduced by at least 30% when compared with a level of ammonia that would exist in the absence of the bacterial strain. The composition is useful for alleviating or preventing the accumulation of ammonia in aqueous environment, e.g. a freshwater or seawater aquarium.

Sequence 1491 BP; 392 A; 323 C; 457 G; 319 T; 0 U; 0 Other;

Query Match 98.2%; Score 1440.2; DB 12; Length 1491;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1464; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

QY 1 TTGATCATGGCTCAGATTGAACGCTGGCGGATGCTTTACACATGCAAGTCGAACGGCAG 60
DB 3 TTGATCATGGCTCAGATTGAACGCTGGCGGATGCTTTACACATGCAAGTCGAACGGCAG 62
QY 61 CACGGGTGCTTGCACCTCTGGTGGCGAGTGGCGGAGTGAATGCAATCGGAACGTGTC 120
DB 63 CACGGGTGCTTGCACCTCTGGTGGCGAGTGGCGGAGTGAATGCAATCGGAACGTGTC 122
QY 121 CAGAAATGGGGGATTAACGCATCGAAAGATGTCTTAATACCGGATATTCCTACGAGGAA 180
DB 123 CAGAAATGGGGGATTAACGCATCGAAAGATGTCTTAATACCGGATATTCCTACGAGGAA 182
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DB 243 GGGGTAAAGGCTTACCAAGGCAACGATCAGTAGTTGGTCTGAGAGGACACCGACACAC 302
QY 301 TGGGATGAGACAGCGGCCAGACTCTACGGAGGCGAGCAGTGGGAAATTTTGGACAATG 360
DB 303 TGGGATGAGACAGCGGCCAGACTCTACGGAGGCGAGCAGTGGGAAATTTTGGACAATG 362
QY 361 GCGGAAGCCTGATCCAGCAATCGCGTGTAGTGAAGAGG-CTTCGGGTTGTAAGCTC 419
DB 363 GCGGAAGCCTGATCCAGCAATCGCGTGTAGTGAAGAGGCTTCGGGTTGTAAGCTC 422
QY 420 TTTTTCAGTCGAGAGAAAGGTTGTGACTAATAATCAACAATTTATGATGGTACCGACAGAA 479
DB 423 TTTTTCAGTCGAGAGAAAGGTTGTGACTAATAATCAACAATTTATGATGGTACCGACAGAA 482
QY 480 GAAGCAGCGGCTAATCTAGTGCAGCAGCGCGGTAATACGTAGGTCGAACGGTTAATC 539
DB 483 GAAGCAGCGGCTAATCTAGTGCAGCAGCGCGGTAATACGTAGGTCGAACGGTTAATC 542
QY 540 GGAATTAATCTGGGCTTAAGGGTGGCGAGCGGCTTTGTAAGTGCAGATGTAAGTCCCGG 599
DB 543 GGAATTAATCTGGGCTTAAGGGTGGCGAGCGGCTTTGTAAGTGCAGATGTAAGTCCCGG 602
QY 600 GCTTAACTCTGGGCTTAAGGGTGGCGAGCGGCTTTGTAAGTGCAGATGTAAGTCCCGG 659
DB 603 GCTTAACTCTGGGCTTAAGGGTGGCGAGCGGCTTTGTAAGTGCAGATGTAAGTCCCGG 662
QY 660 TTCCATGTGTAGCAGTGAATTCGCTAGAGATATGGAAGAAATCGATGGCGAAGCGACCC 719
DB 663 TTCCATGTGTAGCAGTGAATTCGCTAGAGATATGGAAGAAATCGATGGCGAAGCGACCC 722
QY 720 CCCTGGGTTTAACTGACGCTCATCGACGAAGCGTGGGAGCAACAGGATTTAGATACC 779
DB 723 CCCTGGGTTTAACTGACGCTCATCGACGAAGCGTGGGAGCAACAGGATTTAGATACC 782
QY 780 CTGGTAGTCCACGCCCTTAACGATGTCAACTAGTTGTTGGGCTTTACTAGGCTTGGTAAC 839

DB 783 CTGGTAGTCCACGCCCTAAACGATGTCAACTAGTTGTTGGGCTTTACTAGGCTTGGTAAC 842
QY 840 GTACTAACCGGTGAAGTTGACCGCTGGGGAGTACGGTCGACAGATTAAACCTCAGAGG 899
DB 843 GTACTAACCGGTGAAGTTGACCGCTGGGGAGTACGGTCGACAGATTAAACCTCAGAGG 902
QY 900 AATTGACGGGGACCCCGCACAGCGGTGGATTATGTTGGATTAAATTCGATGCAACGCGAATA 959
DB 903 AATTGACGGGGACCCCGCACAGCGGTGGATTATGTTGGATTAAATTCGATGCAACGCGAATA 962
QY 960 ACTTACTACCTTGCATGATGACGAATATTTAGAGATAAATAGTGCCTTCGGGAAC 1019
DB 963 ACTTACTACCTTGCATGATGACGAATATTTAGAGATAAATAGTGCCTTCGGGAAC 1022
QY 1020 GCTAACACAGTGTGCTGATGGCTGTGTCAGCTGTGTCGAGATGTTGGGTTAAGTCC 1079
DB 1023 GCTAACACAGTGTGCTGATGGCTGTGTCAGCTGTGTCGAGATGTTGGGTTAAGTCC 1082
QY 1080 CGCAACGAGCGCAACCCCTTGTCAATTAATTTGTCATCATTTAGTTGGGCACTTTAATGAGAC 1139
DB 1083 CGCAACGAGCGCAACCCCTTGTCAATTAATTTGTCATCATTTAGTTGGGCACTTTAATGAGAC 1142
QY 1140 TGGCGGTGACAAACCGGAGGAGGTGGGATGACGTCAAGTCTCTCATGGCCCTTATGGGT 1199
DB 1143 TGGCGGTGACAAACCGGAGGAGGTGGGATGACGTCAAGTCTCTCATGGCCCTTATGGGT 1202
QY 1200 AGGCTTTTACACGTAATCAATGCGCGGTACAGAGGTTGCCAACCCCGGAGGGGAGCT 1259
DB 1203 AGGCTTTTACACGTAATCAATGCGCGGTACAGAGGTTGCCAACCCCGGAGGGGAGCT 1262
QY 1260 AATCTCAGAAAGCGCGTCTGATCCGGATCCGAGTCTGCAACTCGACTCCGCTGAAGTCGG 1319
DB 1263 AATCTCAGAAAGCGCGTCTGATCCGGATCCGAGTCTGCAACTCGACTCCGCTGAAGTCGG 1322
QY 1320 AATCGTAGTAATCGCGGATCAGCATGTGCGGGTGAATACGTTCCCGGGTCTTGTACACA 1379
DB 1323 AATCGTAGTAATCGCGGATCAGCATGTGCGGGTGAATACGTTCCCGGGTCTTGTACACA 1382
QY 1380 CCGCCCGTCAACCATGGGAGTGGTTCACCAAGCAGATAGTCTAACCGTAA-GAGG 1438
DB 1383 CCGCCCGTCAACCATGGGAGTGGTTCACCAAGCAGATAGTCTAACCGTAA-GAGG 1438
QY 1439 GCGTTTGCACCGCGGAGATTTCATGACTGG 1467
DB 1443 GCGTTTGCACCGCGGAGATTTCATGACTGG 1471

RESULT 3
ADM32722
ID ADM32722 standard; DNA; 1494 BP.
XX ADM32722;
XX
XX 17-JUN-2004 (first entry)
XX AOB P4clone31 16S rDNA.
XX
XX 16S rDNA; ammonia oxidising bacteria; AOB; ammonia; nitrite;
KW aqueous environment; freshwater; seawater; aquarium; ss.
XX Nitrosomonas aestuarii.
XX
XX WO2004026772-A2.
XX
XX 01-APR-2004.
XX
XX 10-SEP-2003; 2003WO-US028210.
XX
XX 19-SEP-2002; 2002US-0386217P.
PR 19-SEP-2002; 2002US-0386218P.
PR 19-SEP-2002; 2002US-0386219P.
XX
XX (AQUA-) AQUARIA INC.

XX	Hovanec TÅ;
PI	
XX	WPI; 2004-304936/2B.
DR	
XX	New composition comprising an isolated bacterial strain that oxidizes
PT	ammonia to nitrite, useful for alleviating or preventing the accumulation
PT	of ammonia in aqueous environment.
XX	
XX	Claim 1; Page 14; 98pp; English.
PS	
XX	This sequence represents a 16S rDNA sequence derived from an ammonia
CC	oxidizing bacteria (AOB). This sequence may be used in a composition
CC	which comprises an isolated bacterial strain that oxidizes ammonia to
CC	nitrite. The composition may be used for alleviating or preventing the
CC	accumulation of ammonia in a medium. The ammonia is reduced by at least
CC	30% when compared with a level of ammonia that would exist in the absence
CC	of the bacterial strain. The composition is useful for alleviating or
CC	preventing the accumulation of ammonia in aqueous environment, e.g. a
CC	freshwater or seawater aquarium.
XX	
SQ	Sequence 1494 BP; 392 A; 327 C; 459 G; 316 T; 0 U; 0 Other;
Query Match 95.7%; Score 1403.4; DB 12; Length 1494;	
Best Local Similarity 98.1%; Pred. No. 0;	
Matches 1441; Conservative 0; Mismatches 26; Indels 2; Gaps 2;	
Qy	1 TTGATCATGGCTCAGATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACGGCAG 60
Db	
Qy	4 TTGATCATGGCTCAGATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACGGCAG 63
Db	
Qy	61 CACGGGTGCTTTGCACCTGGTGGCGAGTGGCGGAGTGAGTAATGCATTCGGAACGTGTC 120
Db	
Qy	64 CACGGGTGCTTTGCACCTGGTGGCGAGTGGCGGAGTGAGTAATGCATTCGGAACGTGTC 123
Db	
Qy	121 CAGAACTGGGGGATTAACGCATCGAAGATGTCTTAATACCGCATATCTCTACGGAGGAA 180
Db	
Qy	124 CGGAAGTGGGGGATTAACGCATCGAAGATGTCTTAATACCGCATATCTCTACGGAGGAA 183
Db	
Qy	181 AGCAGGGGATCGAAAGACCTTTGTGCTTTTGGAGCGCGCGATGCCCTGATTAGCTAGTGGT 240
Db	
Qy	184 AGCAGGGGATCGAAAGACCTTTGTGCTTTTGGAGCGCGCGATGCCCTGATTAGCTAGTGGT 243
Db	
Qy	241 GGGGTAAAGGGCTTACCAAGGCNAACGATCAGTAGTTGGTCTGAGAGGACGACCGACAC 300
Db	
Qy	244 GGGGTAAAGGGCTTACCAAGGCNAACGATCAGTAGTTGGTCTGAGAGGACGACCGACAC 303
Db	
Qy	301 TGGGACTGAGACACGGSCCAGACTCTCAGGAGGCGCAGTCAGTGGGGAAATTTTGGACAATG 360
Db	
Qy	304 TGGGACTGAGACACGGSCCAGACTCTCAGGAGGCGCAGTCAGTGGGGAAATTTTGGACAATG 363
Db	
Qy	361 GCGGAAAGCCTGATCAGCAATGCCGCTGAGTGAAGAAGG-CTTCGGGTGTTGAAGCTC 419
Db	
Qy	364 GCGGAAAGCCTGATCCAGCAATGCCGCTGAGTGAAGAAGGCTTCGGGTGTTGAAGCTC 423
Db	
Qy	420 TTTTCACTCGAAGAAGAAAGTTTGCACTTAATATCACAACCTTATGATGTTACCGACAGAA 479
Db	
Qy	424 TTTTCACTCGAAGAAGAAAGTTTGCACTTAATATCACAACCTTATGATGTTACCGACAGAA 483
Db	
Qy	480 GAAGCACCGGCTAACTCAGTGGCAGCAGCGCGGTAAATACGTAAGGTCAAGCGTTAATC 539
Db	
Qy	484 GAAGCACCGGCTAACTCAGTGGCAGCAGCGCGGTAAATACGTAAGGTCAAGCGTTAATC 543
Db	
Qy	540 GGAAATTAATGCGGCGTAAAGGTTGCGGAGCGCGCTTTGTAAGTCAGATGTGAATATCCCGG 599
Db	
Qy	544 GGAAATTAATGCGGCGTAAAGGTTGCGGAGCGCGCTTTGTAAGTCAGATGTGAATATCCCGG 603
Db	
Qy	600 GCTTAACCTGGGAAATTTGCGTTTGAAACTACAAGCTAGAGTGTAGCAGAGGGGGGTGGAA 659
Db	
Qy	604 GCTTAACCTGGGAAATTTGCGTTTGAAACTACAAGCTAGAGTGTAGCAGAGGGGGGTGGAA 663
Db	
Qy	660 TTCCATGTGTAGCAGTGAAATCGGTAGAGATATGGAAGAACATCGATGCGGAAGGCGGCC 719
Db	

XX PD 29-NOV-2001.
 XX PF 17-MAY-2001; 2001WO-US016265.
 XX PR 19-MAY-2000; 2000US-00573684.
 XX PA (AQUA-) AQUARIA INC.
 XX PI Hovanec TA, Burrell PC;
 XX DR WPI; 2002-075367/10.
 XX PT New bacteria capable of oxidizing ammonia to nitrite, for preventing or
 PT alleviating the accumulation of ammonia in fresh water aquaria, seawater
 PT aquaria and waste water.
 XX PS Claim 2; Page 5; 62pp; English.
 CC The invention relates to 4 novel types of ammonia-oxidising bacteria
 CC (AOB) found in freshwater aquaria. The bacteria are able to oxidise
 CC ammonia to nitrite and are members of the ammonia-oxidising bacteria
 CC family of the beta subdivision of Proteobacteria. The 4 types of bacteria
 CC can be distinguished on the basis of their 16S rRNA (ribosomal RNA) gene
 CC sequences (ABA02416-ABA02419), and are classified as AOB type A (e.g.,
 CC R7clone140), type A1 (e.g., R7clone187), type B (e.g., R3clone5) and type
 CC C (e.g., R3clone47). The invention also encompasses isolated 16S rRNA
 CC gene sequences of the ammonia-oxidising bacteria of the invention,
 CC oligonucleotide probes and primers for the detection of these bacteria,
 CC and compositions comprising the bacteria. The bacteria of the invention
 CC are useful in biological filters for reducing ammonia accumulation in
 CC both freshwater and seawater aquaria. They may also be used in waste
 CC water treatment and in bioremediation processes to reduce the level of
 CC pollution caused by ammonia. The present sequence represents R7clone140,
 CC a 16S rRNA gene sequence from the type A ammonia-oxidising bacterium of
 CC the invention. (Updated on 29-AUG-2003 to standardise OS field)
 XX SQ Sequence 1457 BP; 378 A; 315 C; 456 G; 308 T; 0 U; 0 Other;

Query Match 92.6%; Score 1358.8; DB 6; Length 1457;
 Best Local Similarity 97.2%; Pred. No. 0;
 Matches 1414; Conservative 0; Mismatches 37; Indels 3; Gaps 3;

QY 16 ATTGAACGCTGGCGGCGGCTTTACATGCAATCGAAGCGGACGAGCGGTGCTGCAC 75
 DB 1 ATTGAACGCTGGCGGCGGCTTTACATGCAATCGAAGCGGACGAGCGGTGCTGCAT 60
 QY 76 CTGCTGGCGAGTGGCGGACGCGGTGAGTAATGCAATCGGAACTGTCAGAGTGGGGGATA 135
 DB 61 CTGCTGGCGAGTGGCGGACGCGGTGAGTAATGCAATCGGAACTGTCAGAGAGGGGGGTA 120
 QY 136 ACGCATCGAAAGATGTGCTAATACCGCATATCTCTACGGAGGAAAGCAGGGGATCGAAA 195
 DB 121 ACGCATCGAAAGATGTGCTAATACCGCATATCTCTAAGGAGGAAAGCAGGGGATCGAAA 180
 QY 196 GACCTTGTGCTTTTGGAGCGCCGATGCTGCTGATGCTAGTGTGGGTAAAGCCCTAC 255
 DB 181 GACCTTGTGCTTTTGGAGCGCCGATGCTGCTGATGCTAGTGTGGGTAAAGCCCTAC 240
 QY 256 CAAGCGCAACGATCAGTAGTGTGCTGCTGAGAGGACGACGACACTGGGACTGAGACACG 315
 DB 241 CAAGCGCGACGATCAGTAGTGTGCTGCTGAGAGGACGACGACACTGGGACTGAGACACG 300
 QY 316 GCCCAGACTCTCTA CGGAGGCGAGTGGGAAATTTTGGACAAATGGGCGAAAGCCTGATC 375
 DB 301 GCCCAGACTCTCTA CGGAGGCGAGTGGGAAATTTTGGACAAATGGGCGCAAGCCTGATC 360
 QY 376 CAGCAATGCCCGGTGAGTAGAGAGG-CTTTCGGGTGTAAGCTCTTTTCAGTCGAGAGA 434
 DB 361 CAGCAATGCCCGGTGAGTAGAGAGGCTTCGGGTGTAAGCTCTTTTCAGTCGAGAGA 420
 QY 435 AAAGGTGTGTAATAATAATCACTTATGATGTTACCGACAGAAAGACCGGCTTAAC 494

DB 421 AAAGGTTCGCGTAAATAATCGTGACTCATGACGGTATCGACAGAAAGACACCGGCTAAC 480
 QY 495 TAGTGCACAGCGCGGCTTAATACGTAGGGTCAAGCGTAAATCGGAAATTTACTGGCGGT 554
 DB 481 TAGTGCACAGCGCGGCTTAATACGTAGGGTCAAGCGTAAATCGGAAATTTACTGGCGGT 540
 QY 555 AAAGGGTGGCGCAGCGCGCTTTGTAAGTCAGATGTGAATCCCGGGCTTAACCTGGGAAT 614
 DB 541 AAAGGGTGGCGCAGCGCGCTTTGTAAGTCAGATGTGAATCCCGGGCTTAACCTGGGAAT 600
 QY 615 TGGCTTTGAAACTACAAAGCTAGAGTGTAGAGGAGGGGTGGAATTTCCATGTAGCAG 674
 DB 601 TGGCTTTGAAACTACAAAGCTAGAGTGTAGAGGAGGGGTGGAATTTCCATGTAGCAG 660
 QY 675 TGAATTCGCTAGAGATATGAAGAACATCGATGCGGAGGAGCGCCCTCGGTTAAACACT 734
 DB 661 TGAATTCGCTAGAGATATGAAGAACATCGATGCGGAGGAGCGCTCTCGGTTAAACACT 720
 QY 735 GAGCTCATGACGAAAGCGTGGGGAGCAAAACAGGATTAGATACCTTGGTAGTCCAGGCC 794
 DB 721 GAGCTCATGACGAAAGCGTGGGGAGCAAAACAGGATTAGATACCTTGGTAGTCCAGGCC 780
 QY 795 CTAACGATCTCAACTAGTTGTTGGGCTTTACTAGGCTTGGTAACTAGCTAACGCGTGA 854
 DB 781 CTAACGATCTCAACTAGTTGTTGGGCTTTACTAGGCTTGGTAACTAGCTAACGCGTGA 840
 QY 855 AGTTGACCGCTGGGGAGTACGCTGCGAGGATTAATACTCAAGGATTTGACGGGGACCC 914
 DB 841 AGTTGACCGCTGGGGAGTACGCTGCGAGGATTAATACTCAAGGATTTGACGGGGACCC 900
 QY 915 GCACAGCGGTGGATTATGTGGATTAATTCGATGCAACGGGAAACCTTTACTACCTCTT 974
 DB 901 GCACAGCGGTGGATTATGTGGATTAATTCGATGCAACGGGAAACCTTTACTACCTCTT 960
 QY 975 GACATGTAGCGAATATTTTATAGATATAAATAGTGCCTTTCGGGAACTGTAACAGAGTGT 1034
 DB 961 GACATGTAGCGAATATTTTATAGATATAAATAGTGCCTTTCGGGAACTGTAACAGAGTGT 1019
 QY 1035 GCATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1094
 DB 1020 GCATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1079
 QY 1095 CTTTGTCAATTAATTTGCCATCATTTAGTTGGGCACTTTAATGAGACTGCCGGTGAACAAAC 1154
 DB 1080 CTTTGTCAATTAATTTGCCATCATTTAGTTGGGCACTTTAATGAGACTGCCGGTGAACAAAC 1139
 QY 1155 GAGGAGAGTGGGATGACGTCAAGTCTCATGCGCCCTTATGCGTACGGGCTTTCACAGTA 1214
 DB 1140 GAGGAGAGTGGGATGACGTCAAGTCTCATGCGCCCTTATGCGTACGGGCTTTCACAGTA 1199
 QY 1215 ATACATGGCGCGTACAGAGGTTGCCAACCCCGGAGGGGAGCTAATCTCAGAAAGGC 1274
 DB 1200 ATACATGGCGCGTACAGAGGTTGCCAACCCCGGAGGGGAGCTAATCTCAGAAAGGC 1259
 QY 1275 GTGCTAGTCCGGATCGGAGTCTGCAACTCGACTCCGTAAGTCCGAAATCGTACTAATCG 1334
 DB 1260 GTGCTAGTCCGGATCGGAGTCTGCAACTCGACTCCGTAAGTCCGAAATCGTACTAATCG 1319
 QY 1335 CGGATCAGCATGTGCGCGTGAATACGTTCCCGGTCTTTGTACACACCGCGCTCACACCA 1394
 DB 1320 CGGATCAGCATGTGCGCGTGAATACGTTCCCGGTCTTTGTACACACCGCGCTCACACCA 1379
 QY 1395 TGGAGTGGGTTTCCACGAGAGCAGATAGTCTAACCGTAA- GAGGGGCTTTGCCACGGCG 1453
 DB 1380 TGGAGTGGGTTTCCACGAGAGCAGATAGTCTAACCGTAA- GAGGGGCTTTGCCACGGCG 1439
 QY 1454 AGATTCAATGACTGG 1467
 DB 1440 AGATTCAATGACTGG 1453

ID ADM32704 standard; DNA; 1457 BP.
XX
AC ADM32704;
XX
DT 17-JUN-2004 (first entry)
XX
DE AOB Type A R7clone140 16S rDNA.
XX
KW 16S rDNA; ammonia oxidising bacteria; AOB; ammonia; nitrite;
KW aqueous environment; freshwater; seawater; aquarium; ss.
XX
OS Nitrosomonas sp.
XX
FN WO2004026772-A2.
XX
PD 01-APR-2004.
XX
PF 10-SEP-2003; 2003WO-US028210.
XX
PR 19-SEP-2002; 2002US-0386217P.
PR 19-SEP-2002; 2002US-0386218P.
PR 19-SEP-2002; 2002US-0386219P.
XX
PA (AQUA-) AQUARIA INC.
XX
FI Hovanec TA;
XX
DR WPI; 2004-304936/28.
XX
PT New composition comprising an isolated bacterial strain that oxidizes
PT ammonia to nitrite, useful for alleviating or preventing the accumulation
PT of ammonia in aqueous environment.
XX
PS Disclosure; Page 8-9; 98pp; English.
XX
CC This sequence represents a 16S rDNA sequence derived from an ammonia
CC oxidising bacteria (AOB). This sequence may be used in a composition
CC which comprises an isolated bacterial strain that oxidizes ammonia to
CC nitrite. The composition may be used for alleviating or preventing the
CC accumulation of ammonia in a medium. The ammonia is reduced by at least
CC 30% when compared with a level of ammonia that would exist in the absence
CC of the bacterial strain. The composition is useful for alleviating or
CC preventing the accumulation of ammonia in aqueous environment, e.g. a
CC freshwater or seawater aquarium.
XX
SQ Sequence 1457 BP; 378 A; 315 C; 456 G; 308 T; 0 U; 0 Other;
Query Match 92.6%; Score 1358.8; DB 12; Length 1457;
Best Local Similarity 97.2%; Pred. No. 0;
Matches 1414; Conservative 0; Mismatches 37; Indels 3; Gaps 3;
QY 16 ATTGAACGCTGGCGCATGCTTTACATGCAAGTCGAAACGGGACGCGGTGCTTCAC 75
Db 1 ATTGAACGCTGGCGCATGCTTTACATGCAAGTCGAAACGGGACGCGGTGCTTCGAT 60
QY 76 CTGGTGGGAGTGGCGGACGGGTGAGTAATCATCGGAACGTGCCAAGTGGGGGATA 135
Db 61 CTGGTGGGAGTGGCGGACGGGTGAGTAATCATCGGAACGTATCCAGAAAGGGGGGTA 120
QY 136 ACGCATCGAAAGATGTGCTATATACCGCATATTTCTTACGGAGGAAGCAGGGGATCGAAA 195
Db 121 ACGCATCGAAAGATGTGCTATATACCGCATATTTCTTACGGAGGAAGCAGGGGATCGAAA 180
QY 196 GACCTTGTGCTTTTGGAGCGCGATGCTGATGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCT 255
Db 181 GACCTTGTGCTTTTGGAGCGCGATGCTGATGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCT 240
QY 256 CAAAGCGACGATCAGTGTGCTGAGAGGACGACGACGACGACGACGACGACGACGACGACG 315
Db 241 CAAAGCGACGATCAGTGTGCTGAGAGGACGACGACGACGACGACGACGACGACGACGACG 300
QY 316 GCCCAGACTCTTACCGGAGGACGACGATGGGGAAATTTTGGACAAATGGGGCGAAAGCCTGATC 375

301 GCCCAGACTCTTACCGGAGGACGACGATGGGGAAATTTTGGACAAATGGGGCGCAAGCCTGATC 360
QY 376 CAGCAATGCCGCTGAGTGAAGAAGG-CTTCGGGTTGTAAAGCTCTTTTCAGTTCGAGAAGA 434
Db 361 CAGCAATGCCGCTGAGTGAAGAAGGCTTCGGGTTGTAAAGCTCTTTTCAGTTCGAGAAGA 420
QY 435 AAAGGTTGTGACTTAATAATCAAACTTATGATGGTACCAGCAGAGAAGACACCGGCTAAC 494
Db 421 AAAGGTTACGGTAAATAATCGTGACTCATGACGGTATCGACAGAAGACACCGGCTAAC 480
QY 495 TACGTGCCAGCAGCCGCGTAAATACGTAGGTTGCAAGCGTTAAATCGGAATTAATCTGGGGT 554
Db 481 TACGTGCCAGCAGCCGCGTAAATACGTAGGTTGCAAGCGTTAAATCGGAATTAATCTGGGGT 540
QY 555 AAAGGTTGCCAGCGCGCTTTGTAAGTCAGATGTAAGTCCCGGGCTTTAACTCTGGGAAT 614
Db 541 AAAGGTTGCCAGCGCGCTTTGTAAGTCAGATGTAAGTCCCGGGCTTTAACTCTGGGAAT 600
QY 615 TCGCTTTGAAACTACAAAGCTAGAGTGTAGCAGAGGGGGTGGAAATTCATGTGTAGCAG 674
Db 601 TCGCTTTGAAACTACAAAGCTAGAGTGTGGCAGAGGGAGTGGAAATTCATGTGTAGCAG 660
QY 675 TGAATTCGCTAGAGATATGGAAGAACATCGATGGCGAAGGAGCCCTGGGTTAACACT 734
Db 661 TGAATTCGCTAGAGATATGGAAGAACATCGATGGCGAAGGAGCCCTGGGTTAACACT 720
QY 735 GAGGCTCATGACGAAAGCGTGGGAGCAAAACAGGATTAGATACCTTGTGTAGTCCACGCC 794
Db 721 GAGGCTCATGACGAAAGCGTGGGAGCAAAACAGGATTAGATACCTTGTGTAGTCCACGCC 780
QY 795 CTAAACGATGTCAACTAGTGTGGGCTTACTAGGCTTGGTAAACGTAAGTAAACGGTGA 854
Db 781 CTAAACGATGTCAACTAGTGTGGGCTTACTAGGCTTGGTAAACGTAAGTAAACGGTGA 840
QY 855 AGTTGACCCCTCGGGAGTACCGTGCAGGATTAACCTCAAGGAATTAAGCGGGGACCC 914
Db 841 AGTTGACCCCTCGGGAGTACCGTGCAGGATTAACCTCAAGGAATTAAGCGGGGACCC 900
QY 915 GCACAAAGCGGTGATTTATGTGATTAATTCGATGCAACCGCAAAACCTTACTACCTTT 974
Db 901 GCACAAAGCGGTGATTTATGTGATTAATTCGATGCAACCGCAAAACCTTACTACCTTT 960
QY 975 GACATGTAGCGAATATTTTAGAGATAAATAGTGCCTTCGGGAACGCTAACACAGGTGCT 1034
Db 961 GACATGTAGCGAATATTTTAGAGATAAATAGTGCCTTCGGGAACGCTAACACAGGTGCT 1019
QY 1035 GCATGCTCTCGTCACTGCTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAAC 1094
Db 1020 GCATGCTCTCGTCACTGCTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAAC 1079
QY 1095 CCTTGTCTTAAATTCGCATCATTTAGTTGGGCATTTAATAGACTGCGCGTGACAAACC 1154
Db 1080 CCTTGTCTTAAATTCGCATCATTTAGTTGGGCATTTAATAGACTGCGCGTGACAAACC 1139
QY 1155 GGAGGAAGTGGGGATGAGTCAAGTCTCATGGCCCTTATGGGTAGGGCTTCACACGTA 1214
Db 1140 GGAGGAAGTGGGGATGAGTCAAGTCTCATGGCCCTTATGGGTAGGGCTTCACACGTA 1199
QY 1215 ATACAATGGCGCTACAGAGGGTTGCAACCCCGAGGGGAGCTAATCTCAGAAAGCGC 1274
Db 1200 ATACAATGGCGCTACAGAGGGTTGCAACCCCGAGGGGAGCTAATCTCAGAAAGCGC 1259
QY 1275 GTCGTAGTCGGATCGGAGTCTCAACTGACTCCCGTGAAGTCGGAATTCGTAGTATCG 1334
Db 1260 GTCGTAGTCGGATCGGAGTCTCAACTGACTCCCGTGAAGTCGGAATTCGTAGTATCG 1319
QY 1335 CGGATCAGCATGTTCGGGTGAATACGTTCCCGGCTTTGTACACACGCGCCGTCACACCA 1394
Db 1320 CGGATCAGCATGTTCGGGTGAATACGTTCCCGGCTTTGTACACACGCGCCGTCACACCA 1379
QY 1395 TGGGAGTGGGTTTCAACCAAGCAGATAGTCTTAACCGCTAA -GAGGGCGTTTGGCAGCGGC 1453
Db 1380 TGGGAGTGGGTTTCAACCAAGCAGATAGTCTTAACCGTAAAGGAGGGCGCTTGGCCAGCGTG 1439

QY 1454 AGATTCATGACTGG 1467
 DB 1440 AGATTCATGACTGG 1453

RESULT 6
 ID ABA02417 standard; DNA; 1457 BP.
 XX ABA02417;
 AC ABA02417;
 XX 29-AUG-2003 (revised)
 DT 04-MAR-2002 (first entry)
 XX Type A1 ammonia-oxidising bacterium 16S rRNA gene sequence, R7clone187.
 XX Type A1; ammonia-oxidising bacterium; AOB; nitrite; 16S rRNA gene;
 KW ribosomal RNA; aquarium; aquaculture; waste water treatment;
 KW bioremediation; ds.
 XX Nitrosomonadales.
 OS WO200190312-A1.
 XX 29-NOV-2001.
 PD 17-MAY-2001; 2001WO-US016265.
 PF 19-MAY-2000; 2000US-00573684.
 PR (AQUA-) AQUARIA INC.
 XX Hovanec TA, Burrell PC;
 PI WPI; 2002-075367/10.
 XX New bacteria capable of oxidizing ammonia to nitrite, for preventing or
 PT alleviating the accumulation of ammonia in fresh water aquaria, seawater
 PT aquaria and waste water.
 XX Claim 2; Page 6; 62pp; English.
 XX The invention relates to 4 novel types of ammonia-oxidising bacteria
 CC (AOB) found in freshwater aquaria. The bacteria are able to oxidise
 CC ammonia to nitrite and are members of the ammonia-oxidising bacteria
 CC family of the beta subdivision of Proteobacteria. The 4 types of bacteria
 CC can be distinguished on the basis of their 16S rRNA (ribosomal RNA) gene
 CC sequences (ABA02416-ABA02419), and are classified as AOB type A (e.g.,
 CC R7clone140), type A1 (e.g., R7clone187), type B (e.g., R3clone5) and type
 CC C (e.g., R3clone47). The invention also encompasses isolated 16S rRNA
 CC gene sequences of the ammonia-oxidising bacteria of the invention,
 CC oligonucleotide probes and primers for the detection of these bacteria,
 CC and compositions comprising the bacteria. The bacteria of the invention
 CC are useful in biological filters for reducing ammonia accumulation in
 CC both freshwater and seawater aquaria. They may also be used in waste
 CC water treatment and in bioremediation processes to reduce the level of
 CC pollution caused by ammonia. The present sequence represents R7clone187,
 CC a 16S rRNA gene sequence from the type A1 ammonia-oxidising bacterium of
 CC the invention. (Updated on 29-AUG-2003 to standardise OS field)
 XX Sequence 1457 BP; 379 A; 317 C; 455 G; 306 T; 0 U; 0 Other;

Query Match 92.5%; Score 1357.2; DB 6; Length 1457;
 Best Local Similarity 97.2%; Pred. No. 0;
 Matches 1413; Conservative 0; Mismatches 38; Indels 3; Gaps 3;

QY 16 ATTGACGCTGGCGCATGCTTTACATGCAAGTCGAACGCGACGACGCGGTGCTTGCAC 75
 DB 1 ATTGAACGCTGGCGCATGCTTTACATGCAAGTCGAACGCGACGCGGTGCTTGCAT 60
 QY 76 CTGGTGGCGAGTGGCGACGCGGTGAGTAAATGCATCGGAACGTGTCCAGAAAGTGGGGGATA 135
 DB 1155 GGAGGAAGGTGGGGATGACGTCGCTCAAGTCTCATGGCCCTTATGGGTAGGGCTTACACGTA 1199

61 CTGGTGGCGAGTGGCGGACGCGGTGAGTAAATGCATCGGAACGTATCCAGAAAGGGGGGTA 120
 QY 136 ACGCATCGAAAGATGCTTAATACCGCATATTTCTACGGAGGAAAGCAGGGGATCGAAA 195
 DB 121 ACGCATCGAAAGATGCTTAATACCGCATATTTCTAAGGAGGAAAGCAGGGGATCGAAA 180
 QY 196 GACCTTGTGCTTTTGGAGCGGCCGATGCTGATTTAGCTAGTTGGTGGGTTAAAGCCCTAC 255
 DB 181 GACCTTGTGCTTTTGGAGCGGCCGATGCTGATTTAGCTAGTTGGTGGGTTAAAGCCCTAC 240
 QY 256 CAAGGCAACGATCAGTAGTGGTCTGAGAGGACGACCAAGCCACACTGGGACTGAGACAG 315
 DB 241 CAAGGCAACGATCAGTAGTGGTCTGAGAGGACGACCAAGCCACACTGGGACTGAGACAG 300
 QY 316 GCCCAGACTCTTACGGGAGCGCAGTGGGGAATTTTGGCAATGGGCGAAGCCTGATC 375
 DB 301 GCCCAGACTCTTACGGGAGCGCAGTGGGGAATTTTGGCAATGGGCGAAGCCTGATC 360
 QY 376 CAGCAATGCCGCGTGAAGTGAAGAGG-C-TTTCGGGTTGTAAAGCTCTTTTCACTCGAAGA 434
 DB 361 CAGCAATGCCGCGTGAAGTGAAGAGGCTTCGGGTTGTAAAGCTCTTTTCACTCGAAGA 420
 QY 435 AAAGTTGTGACTTAATTAATCAAACTTATGATGTACCGACAGAAAGACCGGCTAAC 494
 DB 421 AAAGTTGTGACTTAATTAATCAAACTTATGATGTACCGACAGAAAGACCGGCTAAC 480
 QY 495 TACGTGCCAGCAGCGCGGTAATACGTAGGTGCAAGCGTTAATCGGAATTTACTGGGCGT 554
 DB 481 TACGTGCCAGCAGCGCGGTAATACGTAGGTGCAAGCGTTAATCGGAATTTACTGGGCGT 540
 QY 555 AAAGGTGGCGCAGCGCGCTTTTGAAGTCAGATGTGAATATCCCGGGCTTAACTGGGAAT 614
 DB 541 AAAGGTGGCGCAGCGCGCTTTTGAAGTCAGATGTGAATATCCCGGGCTTAACTGGGAAT 600
 QY 615 TGCCTTTGAAACTACAAAGCTTAGAGTGTGAGAGGGGGTGAATTTCCATGTGTAGCAG 674
 DB 601 TGCCTTTGAAACTACAAAGCTTAGAGTGTGAGAGGGGGTGAATTTCCATGTGTAGCAG 660
 QY 675 TGAATTCGCTAGAGATATGGAAGAACATCGATGCGAGGAGCGCCCTCGGTTAACTACT 734
 DB 661 TGAATTCGCTAGAGATATGGAAGAACATCGATGCGAGGAGCGCCCTCGGTTAACTACT 720
 QY 735 GACGCTCATGCAGAAAGCGTGGGAGCAAAACAGGATTAGATACCTCGTGTAGTCACGCC 794
 DB 721 GACGCTCATGCAGAAAGCGTGGGAGCAAAACAGGATTAGATACCTCGTGTAGTCACGCC 780
 QY 795 CTAAACGATGTCAACTAGTTTGGGCTTATTTAGGCTTGGTAACGAAGCTTAACGCGTGA 854
 DB 781 CTAAACGATGTCAACTAGTTTGGGCTTATTTAGGCTTGGTAACGAAGCTTAACGCGTGA 840
 QY 855 AGTTGACCGCTGGGAGTACGGTTCGAGGATTAATACTCAAGGAATTTGACGGGGACCC 914
 DB 841 AGTTGACCGCTGGGAGTACGGTTCGAGGATTAATACTCAAGGAATTTGACGGGGACCC 900
 QY 915 GCACAAAGCGTGGATTTATGTGGATTAAATCGATGCAACCGGAAACCTTACCTACCTCT 974
 DB 901 GCACAAAGCGTGGATTTATGTGGATTAAATCGATGCAACCGGAAACCTTACCTACCTCT 960
 QY 975 GACATGTAGCGAAATATTTTATAGAGATAAAATAGTGCCTTCGGGAAACGCTTAACAGAGTGT 1034
 DB 961 GACATGTAGCGAAATATTTTATAGAGATAAAATAGTGCCTTCGGGAAACGCTTAACAGAGTGT 1019
 QY 1035 GCATGGCTGTGCTGAGTGTGCTGAGATGTTGGGTAAAGTCCCGCAAGAGCGCAAC 1094
 DB 1020 GCATGGCTGTGCTGAGTGTGCTGAGATGTTGGGTAAAGTCCCGCAAGAGCGCAAC 1079
 QY 1095 CTTTGTCAATTAATTTGCCATCAATTTAGTTGGGCACTTTAAATGAGACTCCCGGTGACAAACC 1154
 DB 1080 CTTTGTCAATTAATTTGCCATCAATTTAGTTGGGCACTTTAAATGAGACTCCCGGTGACAAACC 1139
 QY 1155 GGAGGAAGGTGGGGATGACGTCGCTCAAGTCTCATGGCCCTTATGGGTAGGGCTTACACGTA 1214
 DB 1140 GGAGGAAGGTGGGGATGACGTCGCTCAAGTCTCATGGCCCTTATGGGTAGGGCTTACACGTA 1199

QY 1215 ATACAATGGCGCGTACAGAGGGTTGCCAACCCCGGAGGGGAGCTAATCTCAGAAAGCGC 1274
 DB 1200 ATACAATGGCGCGTACAGAGGGTTGCCAACCCCGGAGGGGAGCTAATCTCAGAAAGCGC 1259
 QY 1275 GTCGTAGTCCGGATCGGAGTCTGCAACTCGACTCCGTTGAAAGTGGAAATCGTAGTAATCG 1334
 DB 1260 GTCGTAGTCCGGATCGGAGTCTGCAACTCGACTCCGTTGAAAGTGGAAATCGTAGTAATCG 1319
 QY 1335 CGGATCAGCATGTCCGGTGAATACGTTCCCGGTCTTTGTACACACCGCCCGTCAACCA 1394
 DB 1320 CGGATCAGCATGTCCGGTGAATACGTTCCCGGTCTTTGTACACACCGCCCGTCAACCA 1379
 QY 1395 TGGAGTGGGTTTCCACAGAGCAGATAGTCTAACCGTAA-GAGGGGTTTGCACGGCG 1453
 DB 1380 TGGAGTGGGTTTCCACAGAGCAGATAGTCTAACCGTAAAGGAGGGGCGCTTGCCACGGTG 1439
 QY 1454 AGATTTCATGACTGG 1467
 DB 1440 AGATTTCATGACTGG 1453

RESULT 7
 ID ADM32705 standard; DNA; 1457 BP.
 XX ADM32705;
 AC ADM32705;
 XX ADM32705;
 DT 17-JUN-2004 (first entry)
 XX AOB Type A1 R7clone187 16S rDNA.
 DE 16S rDNA; ammonia oxidising bacteria; AOB; ammonia; nitrite;
 XX aqueous environment; freshwater; seawater; aquarium; ss.
 KW Nitrosomonas sp.
 OS WO2004026772-A2.
 XX 01-APR-2004.
 XX 10-SEP-2003; 2003WO-US028210.
 XX 19-SEP-2002; 2002US-0386217P.
 PR 19-SEP-2002; 2002US-0386218P.
 PR 19-SEP-2002; 2002US-0386219P.
 XX (AQUA-) AQUARIA INC.
 XX Hovaneq TA;
 PI WPI; 2004-304936/28.
 XX New composition comprising an isolated bacterial strain that oxidizes
 PT ammonia to nitrite, useful for alleviating or preventing the accumulation
 PT of ammonia in aqueous environment.
 XX Disclosure; Page 10; 98pp; English.
 PS This sequence represents a 16S rDNA sequence derived from an ammonia
 XX oxidising bacteria (AOB). This sequence may be used in a composition
 CC which comprises an isolated bacterial strain that oxidizes ammonia to
 CC nitrite. The composition may be used for alleviating or preventing the
 CC accumulation of ammonia in a medium. The ammonia is reduced by at least
 CC 30% when compared with a level of ammonia that would exist in the absence
 CC of the bacterial strain. The composition is useful for alleviating or
 CC preventing the accumulation of ammonia in aqueous environment, e.g. a
 CC freshwater or seawater aquarium.
 XX Sequence 1457 BP; 379 A; 317 C; 455 G; 306 T; 0 U; 0 Other;

Query Match 92.5%; Score 1357.2; DB 12; Length 1457;
 Best Local Similarity 97.2%; Pred. No. 0;

Matches 1413; Conservative 0; Mismatches 38; Indels 3; Gaps 3;
 QY 16 ATTGAACGTCGCGCATGCTTTTACACATGCAAGTCGAACGCGCAGCACGGGTCTTGCAC 75
 DB 1 ATTGAACGTCGCGCATGCTTTTACACATGCAAGTCGAACGCGCAGCACGGGTCTTGCAT 60
 QY 76 CTGGTGGCGAGTGGCGGACGGGTGAGTAAATGTCATCGGAACGTCGTCCAGAAGTGGGGATA 135
 DB 61 CTGGTGGCGAGTGGCGGACGGGTGAGTAAATGTCATCGGAACGTCGTCCAGAAGTGGGGATA 120
 QY 136 AGCATCGAAAGATGTCCTAATACCGCATATTTCTCTACGAGGAAAGCAGGGGATCGAAA 195
 DB 121 AGCATCGAAAGATGTCCTAATACCGCATATTTCTCTAAGGAGGAAAGCAGGGGATCGAAA 180
 QY 196 GACCTTGTCTTTTGGAGCGCGCATGCTGATTAAGTCTAGTCTGGTGGGTAAAGGCTTAC 255
 DB 181 GACCTTGTCTTTTGGAGCGCGCATGCTGATTAAGTCTAGTCTGGTGGGTAAAGGCTTAC 240
 QY 256 CAAGGCAACGATCAGTAGTTGGTCTGAGAGGACGACCACTGGGACTGAGACAG 315
 DB 241 CAAGGCGACGATCAGTAGTTGGTCTGAGAGGACGACCACTGGGACTGAGACAG 300
 QY 316 GCCAGACTCTTACCGGAGGCGAGTGGGAAATTTTGGCAATGGGCGCAAGCCCTGATC 375
 DB 301 GCCAGACTCTTACCGGAGGCGAGTGGGAAATTTTGGCAATGGGCGCAAGCCCTGATC 360
 QY 376 CAGCAATGCGCGTGAAGTGAAGGAGG-CTTTCGGGTGTTAAAGCTCTTTCAGTCGAGAAGA 434
 DB 361 CAGCAATGCGCGTGAAGTGAAGGAGGCTTTCGGGTGTTAAAGCTCTTTCAGTCGAGAAGA 420
 QY 435 AAAGGTTGTGACTTAATAATCAAACTTATGATGGTACCAAGAGAACGACCGGCTAAC 494
 DB 421 AAAGGTTGTGACTTAATAATCAAACTTATGATGGTACCAAGAGAACGACCGGCTAAC 480
 QY 495 TAGTCCGAGCGCGCGGTGAATACGTCAGGTCGAGCGTAAATCGGAATTTACTGGGCGT 554
 DB 481 TAGTCCGAGCGCGCGGTGAATACGTCAGGTCGAGCGTAAATCGGAATTTACTGGGCGT 540
 QY 555 AAAGGTCGCGAGCGCGCTTTTGTAGTCAGATGTGAAATCCCCGGGCTTTAACTGGGAAT 614
 DB 541 AAAGGTCGCGAGCGCGCTTTTGTAGTCAGATGTGAAATCCCCGGGCTTTAACTGGGAAT 600
 QY 615 TCGCTTTGAAACTTACAAAGCTAGAGTGTAGCAGAGGGGGTGAATTCATGTGTAGCAG 674
 DB 601 TCGCTTTGAAACTTACAAAGCTAGAGTGTAGCAGAGGGGGTGAATTTCCATGTGTAGCAG 660
 QY 675 TGAATGCGTAGAGATATGGAAGAACATCGATGCGGAAGCGACGCCCTTGGGTAAACACT 734
 DB 661 TGAATGCGTAGAGATATGGAAGAACATCGATGCGGAAGCGACGCCCTTGGGTAAACACT 720
 QY 735 GACGCTCATGCGAAGCGTGGGAGCAAAACAGGATTTAGATACCTCTGGTAGTCCAGGCC 794
 DB 721 GACGCTCATGCGAAGCGTGGGAGCAAAACAGGATTTAGATACCTCTGGTAGTCCAGGCC 780
 QY 795 CTAACGATGTCAACTAGTTGTTGGGCTTACTAGGCTTGGTAACTAGCTAGCTAACGGTGA 854
 DB 781 CTAACGATGTCAACTAGTTGTTGGGCTTACTAGGCTTGGTAACTAGCTAGCTAACGGTGA 840
 QY 855 AGTTGACCGCTGGGAGTACGGTCCAGGATTTAAATCTCAAAAGGAATTCACCGGGACCC 914
 DB 841 AGTTGACCGCTGGGAGTACGGTCCAGGATTTAAATCTCAAAAGGAATTCACCGGGACCC 900
 QY 915 GCACAGCGGTGATTAATGTGGATTAATTCGATGCAACGCGAAGAAACCTTACCTACCCCTT 974
 DB 901 GCACAGCGGTGATTAATGTGGATTAATTCGATGCAACGCGAAGAAACCTTACCTACCCCTT 960
 QY 975 GACATGTAGGGAATATTTAGATATAAATAGTGCCTTCGGGAACGCTAACACAGGTGCT 1034
 DB 961 GACATGTAGGGAATATTTAGATATAAATAGTGCCTTCGGGAACGCTAACACAGGTGCT 1019
 QY 1035 GCATGGCTGTCGTCAGCTCGTGTGAGATGTTGGGTAAAGTCCCGCAACGAGCGCAAC 1094
 DB 1020 GCATGGCTGTCGTCAGCTCGTGTGAGATGTTGGGTAAAGTCCCGCAACGAGCGCAAC 1079

QY 1095 CCTTGTCTTAATTTGCCATCATTTAGTTGGGCACCTTTAATGAGACTGCGGTGACAAACC 1154
 DB |||||
 QY 1080 CTTTGTCTTAATTTGCCATCATTTTGGTTGGGCACCTTTAATGAGACTGCGGTGACAAACC 1139
 DB |||||
 QY 1155 GGAGGAAGTGGGGATGACGTCAGTCTCATGTGCGCCCTTATGGTAGGGCTTTCACACGTA 1214
 DB |||||
 QY 1140 GGAGGAAGTGGGGATGACGTCAGTCTCATGTGCGCCCTTATGGTAGGGCTTTCACACGTA 1199
 DB |||||
 QY 1215 ATACAAATGCGGTACAGAGGGTTGCCAACCGCGAGGGGAGCTAACTCAGAAAGCGC 1274
 DB |||||
 QY 1200 ATACAAATGCGGTACAGAGGGTTGCCAACCGCGAGGGGAGCTAACTCAGAAAGCGC 1259
 DB |||||
 QY 1275 GTCTAGTCCGGATCGGAGTCTGCAACTCGAATCGGTAAGTCCGAATCGTAGTAATCG 1334
 DB |||||
 QY 1260 GTCTAGTCCGGATCGGAGTCTGCAACTCGAATCGGTAAGTCCGAATCGTAGTAATCG 1319
 DB |||||
 QY 1335 CGGATCAGCATGTGCGGTGGAATAGCTTCCCGGGTCTGTACACCGCCGTCACACCA 1394
 DB |||||
 QY 1320 CGGATCAGCATGTGCGGTGGAATAGCTTCCCGGGTCTGTACACCGCCGTCACACCA 1379
 DB |||||
 QY 1395 TGGGAGTGGTTTCCACGAGCAGATAGTCTAACCGTAA-CAGGGCGTTTCCACGGG 1453
 DB |||||
 QY 1380 TGGGAGTGGTTTCCACGAGCAGATAGTCTAACCGTAAAGGAGGGCGCTTGCCACGGTG 1439
 DB |||||
 QY 1454 AGATTTCATGACTGG 1467
 DB |||||
 QY 1440 AGATTTCATGACTGG 1453
 DB |||||

RESULT 8

ABA02418
 ID ABA02418 standard; DNA; 1458 BP.
 XX ABA02418;
 AC ABA02418;
 DT 29-AUG-2003 (revised)
 DT 04-MAR-2002 (first entry)

DE Type B ammonia-oxidising bacterium 16S rRNA gene sequence, R3clone5.

XX Type B; ammonia-oxidising bacterium; AOB; nitrite; 16S rRNA gene;

KW ribosomal RNA; aquarium; aquaculture; waste water treatment;

KW bioremediation; db.

XX Nitrosomonadales.

XX WO200190312-A1.

PN 29-NOV-2001.

XX 17-MAY-2001; 2001WO-US016265.

XX 19-MAY-2000; 2000US-00573684.

XX (AQUA-) AQUARIA INC.

PI Hovenec TA, Burrell PC;

XX WPI; 2002-075367/10.

PT New bacteria capable of oxidizing ammonia to nitrite, for preventing or
 PT alleviating the accumulation of ammonia in fresh water aquaria, seawater
 PT aquaria and waste water.

PS Claim 2; Page 7; 62pp; English.

CC The invention relates to 4 novel types of ammonia-oxidising bacteria
 CC (AOB) found in freshwater aquaria. The bacteria are able to oxidise
 CC ammonia to nitrite and are members of the ammonia-oxidising bacteria
 CC family of the beta subdivision of Proteobacteria. The 4 types of bacteria
 CC can be distinguished on the basis of their 16S rRNA (ribosomal RNA) gene
 CC sequences (ABA02416-ABA02419), and are classified as AOB type A (e.g.,

CC R7clone140), type A1 (e.g., R7clone187), type B (e.g., R3clone5) and type
 CC C (e.g., R3clone47). The invention also encompasses isolated 16S rRNA
 CC gene sequences of the ammonia-oxidising bacteria of the invention,
 CC oligonucleotide probes and primers for the detection of these bacteria,
 CC and compositions comprising the bacteria. The bacteria of the invention
 CC are useful in biological filters for reducing ammonia accumulation in
 CC both freshwater and seawater aquaria. They may also be used in waste
 CC water treatment and in bioremediation processes to reduce the level of
 CC pollution caused by ammonia. The present sequence represents R3clone5, a
 CC 16S rRNA gene sequence from the type B ammonia-oxidising bacterium of the
 CC invention. (Updated on 29-AUG-2003 to standardise OS field)

XX Sequence 1458 BP; 368 A; 342 C; 466 G; 282 T; 0 U; 0 Other;

QY Query Match 85.3%; Score 1252; DB 6; Length 1458;

DB Best Local Similarity 93.1%; Pred. No. 0;

DB Matches 1355; Conservative 0; Mismatches 95; Indels 6; Gaps 4;

QY 16 ATTGAACGCTGGCGCATGCTTTACACATGCAAGTCGAACGCGCAGCGGTGCTTGCAC 75

DB 1 ATTGAACGCTGGCGCATGCTTTACACATGCAAGTCGAACGCGCAGCGGTGCTTGCAC 58

QY 76 CTGFTGGCAGTGGCGGACGGGTGAGTAATGCAATCGGAACGCTGTCAGAAATGGGGGATA 135

DB 59 CTGFTGGCAGTGGCGGACGGGTGAGTAATGCAATCGGAACGCTGTCAGAAATGGGGGATA 118

QY 136 ACGCATCGAAGATGCTGCTAATACCGCATATCTCTACGAGGAAAGCAGGGGATCGAA 195

DB 119 ACGCACCGAAGATGCTGCTAATACCGCATATCTCTACGAGGAAAGCAGGGGATCGCA 178

QY 196 GACCTTGTGCTTTTGGAGCGGCGATGCTGCTAGTGTAGTTGGTGGGTAAAGGCTTAC 255

DB 179 GACCTTGTGCTTTTGGAGCGGCGATGCTGCTAGTGTAGTTGGTGGGTAAAGGCTTAC 238

QY 256 CAAGCAACGATCAGTAGTGTCTGAGAGGACGACCAAGCCACACTGGGACGTGAGACAG 315

DB 239 CAAGCGCAGATCAGTAGTGTCTGAGAGGACGACCAAGCCACACTGGGACGTGAGACAG 298

QY 316 GCCCAGACTCTACGGGAGGCGAGGTGGGGAATTTTGGCAATGGGGGAAAGCCTGATC 375

DB 299 GCCCAGACTCTCTACGGGAGGCGAGGTGGGGAATTTTGGCAATGGGGGAAAGCCTGATC 358

QY 376 CAGCAATGCCCGCTGAGTGAAGAAAGG-CTTCGGGTGTAAAGCTCTTTCAGTTCGAGAAAG 434

DB 359 CAGCAATGCCCGCTGAGTGAAGAAAGGCTTTCGGGTGTAAAGCTCTTTCAGTTCGAGAAAG 418

QY 435 AAAGTGTGTGCTAATATCAACTTAATGATGTACCGACAGAAAGACCGGCTTAAC 494

DB 419 AACGGTCAACGGCTAATACCGGCTACTGACGGGTACCGGAAGAAAGACCGGCTTAAC 478

QY 495 TACGTGCCAGCAGCGCGGTAAATACGTAGGTGCAAGCGTTAAATCGGAATTAATCGGGCGT 554

DB 479 TACGTGCCAGCAGCGCGGTAAATACGTAGGTGCAAGCGTTAAATCGGAATTAATCGGGCGT 538

QY 555 AAAGGTGCGCAGCGCGCTTTGTAAAGTCAGATGTGAATATCCCGGGCTTAACTCGGGAAT 614

DB 539 AAAGGTGCGCAGCGCGCTTTGTAAAGTCAGATGTGAATATCCCGGGCTTAACTCGGGAAT 598

QY 615 TCGTTTGAACCTCAAAAGCTAGAGTGTAGCAGAGGGGGGTGGAATTCATGTGTAGCAG 674

DB 599 TCGTTTGAACCTCAAAAGCTAGAGTGTAGCAGAGGGGGGTGGAATTCATGTGTAGCAG 658

QY 675 TGAATCGGTAGATATGGAAGACATCCGATGCGGAGGCGAGCCCTCGGGTTAACTACT 734

DB 659 TGAATCGGTAGATATGGAAGACATCCGATGCGGAGGCGAGCCCTCGGGTTAACTACT 718

QY 735 GACGCTCATGCAAGAAAGCGTGGGAGCAAAACAGATTTAGATACCTCGGTAGTCACGCC 794

DB 719 GACGCTCATGCAAGAAAGCGTGGGAGCAAAACAGATTTAGATACCTCGGTAGTCACGCC 778

QY 795 CTAACGATGTCAACTAGTTTGGGCGCTTACTAGGCTTGGTAAAGTAAAGCTAAAGCGTGA 854

DB 779 CTAACGATGTCAACTAGTTTGGGCGCTTACTAGGCTTGGTAAAGTAAAGCTAAAGCGTGA 838

855 AGTTGACCGCTGGGAGTACGGTCGACGATTAATACTCAAAAGGAATTGACGGGACCC 914
|||||
839 AGTTGGCGCCTGGGAGTACGGTCGCAAGTAAATACTCAAGGAATTGACGGGACCC 898
|||||
915 GCACAAGCGGTGGATTATGTGGATTAAATCGATGCAACCGGAAACCTTACCTACCTTT 974
|||||
899 GCACAAGCGGTGGATTATGTGGATTAAATCGATGCAACCGGAAACCTTACCTACCTTT 958
|||||
975 GACATGTAGCGAATATTTAGAGATATAAATAGTGCC--TTCCGGAAACGCTAAACACAGGTG 1032
|||||
959 GACATGTAGCGAATATTTAGAGATATAAATAGTGCC--TTCCGGAAACGCTAAACACAGGTG 1018
|||||
1033 CTGCATGGCTCTCGTCAGCTCGTGTGAGATGTTGGGTTAAAGTCCCGCAACGAGCGCA 1092
|||||
1019 CTGCATGGCTCTCGTCAGCTCGTGTGAGATGTTGGGTTAAAGTCCCGCAACGAGCGCA 1078
|||||
1093 ACCCTTGTCAATAATGCGCATATTTAGTTGGGCACTTTAATGAGACTGCGGTGACAAA 1152
|||||
1079 ACCCTTGTCAATAATGCGCATATTTAGTTGGGCACTTTAATGAGAACTGCGGTGACAAA 1138
|||||
1153 CCGGAGGAAGGTGGGATGAGCTCAAGTCCTCATGGCCCTTATGGGTAGGGCTTTCACACG 1212
|||||
1139 CCGGAGGAAGGTGGGATGAGCTCAAGTCCTCATGGCCCTTATGGGTAGGGCTTTCACACG 1198
|||||
1213 TAATACAAATGGCGGTACAGAGGGTTGCCAAACCCGAGGGGGAGCTAAATCTCAGAAAGC 1272
|||||
1199 TAATACAAATGGCGGTACAGAGGGTTGCCAAACCCGAGGGGGAGCTAAATCTCAGAAAGC 1258
|||||
1273 GCGTCGTAGTCGGATCGGAGTCTGCAACTCGACTCGCTCGTGAAGTCGGAATCGCTAGTAAT 1332
|||||
1259 GCGTCGTAGTCGGATCGGAGTCTGCAACTCGACTCGCTCGTGAAGTCGGAATCGCTAGTAAT 1318
|||||
1333 CGCGATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTCACACACCGCCGCTCACAC 1392
|||||
1319 CCGGATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTCACACACCGCCGCTCACAC 1378
|||||
1393 CATGGAGTGGGTTTCAACAGAGCAGATAGTCTAAACCGTAA--GAGGGCGTTTCCACGG 1451
|||||
1379 CATGGAGTGGGTTTCAACAGAGCAGATAGTCTAAACCGAGGAGTCTAACCGCAGGAGGCGCTTCCACGG 1438
|||||
1452 CGAGATTCATGACTGG 1467
|||||
1439 TGAGATTCATGACTGG 1454
|||||

RESULT 9

ADM32706

ID ADM32706 standard; DNA; 1458 BP.

XX ADM32706;

XX AC

XX DT

XX 17-JUN-2004 (first entry)

XX DE

XX AOB Type B R3clone5 16S rDNA.

XX KW

XX 16S rDNA; ammonia oxidising bacteria; AOB; ammonia; nitrite;

XX KW

XX aqueous environment; freshwater; seawater; aquarium; ss.

XX OS

XX Nitrosomonas sp.

XX XX

XX WO2004026772-A2.

XX PD

XX 01-APR-2004.

XX XX

XX 10-SEP-2003; 2003WO-US028210.

XX XX

XX 19-SEP-2002; 2002US-0386217P.

XX PR

XX 19-SEP-2002; 2002US-0386218P.

XX PR

XX 19-SEP-2002; 2002US-0386219P.

XX XX

XX (AQUA-) AQUARIA INC.

XX .XX

PI Hovanec TA;

XX XX

XX WPI; 2004-304936/28.

XX XX

PT New composition comprising an isolated bacterial strain that oxidizes ammonia to nitrite, useful for alleviating or preventing the accumulation of ammonia in aqueous environment.

XX XX

PS Disclosure; Page 11; 98pp; English.

XX XX

CC This sequence represents a 16S rDNA sequence derived from an ammonia oxidising bacteria (AOB). This sequence may be used in a composition to which comprises an isolated bacterial strain that oxidizes ammonia to nitrite. The composition may be used for alleviating or preventing the accumulation of ammonia in a medium. The ammonia is reduced by at least 30% when compared with a level of ammonia that would exist in the absence of the bacterial strain. The composition is useful for alleviating or preventing the accumulation of ammonia in aqueous environment, e.g. a freshwater or seawater aquarium.

XX XX

SQ Sequence 1458 BP; 368 A; 342 C; 466 G; 282 T; 0 U; 0 Other;

Query Match 85.3%; Score 1252; DB 12; Length 1458;

Best Local Similarity 93.1%; Pred. No. 0;

Matches 1355; Conservative 0; Mismatches 95; Indels 6; Gaps 4;

QY 16 ATTGAACGCTGGCGCATGCTTTACACATGCAAGTCGAACGCGCAGCACGGGTGCTTGCAAC 75

DB 1 ATTGAACGCTGGCGCATGCTTTACACATGCAAGTCGAACGCGCAGCACGGGTGCTTGCAAC 58

QY 76 CTGCTGGCAGTGGCGGACGGGTGAGTAAATGCGAATCGGAACGCTGTCGAGAAAGTGGGGATA 135

DB 59 CTGCTGGCAGTGGCGGACGGGTGAGTAAATGCGAATCGGAACGCTGTCGAGAAAGTGGGGATA 118

QY 136 AGCATCGAAAGATGCTTAATACCGCATATTCCTACCGGAGGAGCAGGGGATCGAAA 195

DB 119 ACGCACGAAAGTGTGCTTAATACCGCATATTCCTACCGGAGGAGCAGGGGATCGCAA 178

QY 196 GACCTGTGCTTTGGAGCGCGCATGCTGATAGTCTAGTGTGGTGGGTAAAGGCTTAC 255

DB 179 GACCTGTGCTTTGGAGCGCGCATGCTGATAGTCTAGTGTGGTGGGTAAAGGCTTAC 238

QY 256 CAAAGCAACGATCAGTATGTTGCTGAGAGGACGACACCGCACCTGGGACTGAGACAG 315

DB 239 CAAAGCAACGATCAGTATGTTGCTGAGAGGACGACACCGCACCTGGGACTGAGACAG 298

QY 316 GCCCAGACTCTACGGGAGCGCAGCTGGGGAATTTTGACCAATGGGCGCAAGCCCTGATC 375

DB 299 GCCCAGACTCTACGGGAGCGCAGCTGGGGAATTTTGACCAATGGGCGCAAGCCCTGATC 358

QY 376 CAGCAATGCCCGCTGAGTGAAGAAGG-CTTCGGGTTGTAAAGCTCTTTCAGTCGAGAAGA 434

DB 359 CAGCCATGCCCGCTGAGTGAAGAAGGCTTCGGGTTGTAAAGCTCTTTCAGTCGAGAAGA 418

QY 435 AAAGGTTGTACTTAATAATCAAACTTATGATGGTACCGACAGCAAGACACCGGCTAAC 494

DB 419 AAAGGTTGTACTTAATAATCAAACTTATGATGGTACCGACAGCAAGACACCGGCTAAC 478

QY 495 TAGTGCCAGCAGCGCGGTAATACGTAGGGTGCAAGCGTTAATTCGGAATTACTGGGCGT 554

DB 479 TAGTGCCAGCAGCGCGGTAATACGTAGGGTGCAAGCGTTAATTCGGAATTACTGGGCGT 538

QY 555 AAAGGTTGCGCAGCGCGCTTTTGAAGTCAGATGTGAATATCCCGGGGTTTAACTGGGAAT 614

DB 539 AAAGGTTGCGCAGCGCGCTTTTGAAGTCAGATGTGAATATCCCGGGGTTTAACTGGGAAT 598

QY 615 TGCGTTTGAACCTACAAAGCTAGAGTGTACGAGGGGGGTGGAATTCCTCATGTGTAGCAG 674

DB 599 TGCGTTTGAACCTACAAAGCTAGAGTGTACGAGGGGGGTGGAATTCCTCATGTGTAGCAG 658

QY 675 TGAATCGGTAGAGATATGGAAGAACATCGATGCGGAAGCAGCCCTCGGTTTAACT 734

DB 659 TGAATCGGTAGAGATATGGAAGAACATCGATGCGGAAGCAGCCCTCGGTTTAACT 718

QY 735 GACGCTCATGACGAAAGCGTGGGAGCAAAACAGAGTTAGATACCTCGTAGTCCACGCC 794
 Db |||||
 QY 719 GACGCTCAGGACGAAAGCGTGGGAGCAAAACAGAGTTAGATACCTCGTAGTCCACGCC 778
 Db |||||
 QY 795 CTAACAGATGTCAACTAGTGTGTGGGCTTACTAGGCTTGGTAACTAGCTAACCGGTGA 854
 Db |||||
 QY 779 CTAACAGATGTCAACTAGTGTGTGGGCTTACTAGGCTTGGTAACTAGCTAACCGGTGA 838
 Db |||||
 QY 855 AGTTGACCGCTGGGAGTACGGTCCGAGGATTAATACTCAAGGAATAGCGGGAGCC 914
 Db |||||
 QY 839 AGTTGCGCGCTGGGAGTACGGTCCGAGGATTAATACTCAAGGAATAGCGGGAGCC 898
 Db |||||
 QY 915 GCACAAGCGGTGATATGTGATTAATTCGATGCAACCGGAAACCTTACTACCTCT 974
 Db |||||
 QY 899 GCACAAGCGGTGATATGTGATTAATTCGATGCAACCGGAAACCTTACTACCTCT 958
 Db |||||
 QY 975 GACATGTAGCGAATATTTTAGAGATAAATAGTGCC--TTCCGGAAACGCTAACACAGGTG 1032
 Db |||||
 QY 959 GACATGTACCGAAGCCCGGAGAGGTGGTGTGCCCGAAAGGAGCGGTAAACACAGGTG 1018
 Db |||||
 QY 1033 CTGCATGCTGTCGTCAGCTCGTGTGAGATGTTGGTTAAGTCCCGCAACGAGCGCA 1092
 Db |||||
 QY 1019 CTGCATGCTGTCGTCAGCTCGTGTGAGATGTTGGTTAAGTCCCGCAACGAGCGCA 1078
 Db |||||
 QY 1093 ACCCTTGTCAATTAATGGCATCATTTAGTGGGCACTTTAATGAGACTCGCGGTGACAAA 1152
 Db |||||
 QY 1079 ACCCTTGTCAATTAATGGCATCATTTAGTGGGCACTTTAATGAGAACTGCGCGGTGACAAA 1138
 Db |||||
 QY 1153 CCGGAGGAGGTGGGATGACGCTCAAGTCTCATGGCCCTTATGGGTAGGGCTTCACACG 1212
 Db |||||
 QY 1139 CCGGAGGAGGTGGGATGACGCTCAAGTCTCATGGCCCTTATGGGTAGGGCTTCACACG 1198
 Db |||||
 QY 1213 TAATACATGGCGCTACAGAGGTTGCCAACCCCGAGGGGAGCTAATTCAGAAAGC 1272
 Db |||||
 QY 1199 TAATACATGGCGCTACAGAGGTTGCCAACCCCGAGGGGAGCTAATTCAGAAAGC 1258
 Db |||||
 QY 1273 GCGTGTAGTCGGATCGGAGTCTCAACTCGACTCCGTGAGTCCGGAATCGCTAGTAAT 1332
 Db |||||
 QY 1259 GCGTGTAGTCGGATCGGAGTCTCAACTCGACTCCGTGAGTCCGGAATCGCTAGTAAT 1318
 Db |||||
 QY 1333 CCGGATCAGCATGTCCGGGTGAATACGTTCCCGGGTCTTTGACACACCGCCCGTACAC 1392
 Db |||||
 QY 1319 CCGGATCAGCATGTCCGGGTGAATACGTTCCCGGGTCTTTGACACACCGCCCGTACAC 1378
 Db |||||
 QY 1393 CATGGAGTGGGTTTCAACAGAGCAGATAGTCTAACCGGTAA-GAGGGGTTTGGCCACGG 1451
 Db |||||
 QY 1379 CATGGAGTGGGTTTCAACAGAGCAGATAGTCTAACCGGAGGAGGGGCGCTTGCCACGG 1438
 Db |||||
 QY 1452 CGAGATTCAATGACTGG 1467
 Db |||||
 QY 1439 TGAGATTCAATGACTGG 1454
 Db |||||

RESULT 10
 ABA02419
 ID ABA02419 standard; DNA; 1460 BP.
 XX
 AC ABA02419;
 XX
 DT 29-AUG-2003 (revised)
 DT 04-MAR-2002 (first entry)
 XX
 DE Type C ammonia-oxidising bacterium 16S rRNA gene sequence, R3clone47.
 XX
 KW Type C; ammonia-oxidising bacterium; AOB; nitrite; 16S rRNA gene;
 KW ribosomal RNA; aquarium; aquaculture; waste water treatment;
 KW bioremediation; ds.
 XX
 OS Nitrosomonadales.
 XX
 PN W0200190312-A1.
 XX

PD 29-NOV-2001.
 XX
 PF 17-MAY-2001; 2001WO-US016265.
 XX
 PR 19-MAY-2000; 2000US-00573684.
 XX
 PA (AQUA-) AQUARIA INC.
 XX
 PI Hovanec TA, Burrell PC;
 XX
 DR WPI; 2002-075367/10.
 XX
 PT New bacteria capable of oxidizing ammonia to nitrite, for preventing or
 alleviating the accumulation of ammonia in fresh water aquaria, seawater
 aquaria and waste water.
 XX
 PS Claim 2; Page 8; 62pp; English.
 XX
 CC The invention relates to 4 novel types of ammonia-oxidising bacteria
 (AOB) found in freshwater aquaria. The bacteria are able to oxidise
 ammonia to nitrite and are members of the ammonia-oxidising bacteria
 family of the beta subdivision of Proteobacteria. The 4 types of bacteria
 can be distinguished on the basis of their 16S rRNA (ribosomal RNA) gene
 sequences (ABA02416-ABA02419), and are classified as AOB type A (e.g.,
 R3clone140), type A1 (e.g., R3clone187), type B (e.g., R3clone5) and type
 C (e.g., R3clone47). The invention also encompasses isolated 16S rRNA
 gene sequences of the ammonia-oxidising bacteria of the invention,
 oligonucleotide probes and primers for the detection of these bacteria,
 and compositions comprising the bacteria. The bacteria of the invention
 are useful in biological filters for reducing ammonia accumulation in
 both freshwater and seawater aquaria. They may also be used in waste
 water treatment and in bioremediation processes to reduce the level of
 pollution caused by ammonia. The present sequence represents R3clone47, a
 16S rRNA gene sequence from the type C ammonia-oxidising bacterium of the
 invention. (Updated on 29-AUG-2003 to standardise OS field)
 XX
 SQ Sequence 1460 BP; 388 A; 316 C; 454 G; 302 T; 0 U; 0 Other;
 Query Match 82.5%; Score 1210.6; DB 6; Length 1460;
 Best Local Similarity 92.5%; Pred. No. 0;
 Matches 1350; Conservative 0; Mismatches 99; Indels 10; Gaps 7;
 QY 16 ATTGAACGCTCGGCGCATGCTTTACACATGCAAGTCGAACCGCAGCAGCGGTGCTTGAC 75
 Db |||||
 QY 1 ATTGAACGCTCGGCGCATGCTTTACACATGCAAGTCGAACCGCAGCAGCGGTGCTTGAC 58
 Db |||||
 QY 76 CTGTGGCGAGTGGCGGACGGTGAGTAATGCATCGGAACGTGTCCAGAACTGGGGGATA 135
 Db |||||
 QY 59 CTGCGGCGAGTGGCGAACGGGTGAGTAATACATCGGAACGTGTCTTAAGTGGGGAATA 118
 Db |||||
 QY 136 ACGCATCGAAGATGTGCTAATACCGCATATTTCTACGGAGGAAGCAGGGGATCGAAA 195
 Db |||||
 QY 119 ACGCATCGAAGATGTGCTAATACCGCATATTTCTCTAGGAGGAAGCAGGGGATCGCAA 177
 Db |||||
 QY 196 GACCTTGTGCTTTTGGAGCGCGCATGCTGATTAGCTAGTTGGTGGGTAAAGCGCTAC 255
 Db |||||
 QY 178 GACCTTGTGCTTTAAGGAGCGCGCATGCTGATTAGCTAGTTGGTGGGTAAAGCGCTAC 237
 Db |||||
 QY 256 CAAGGCAACGATCAGTAGTGGTCTGAGAGGACGACCGACCACTGGGACTGAGACACG 315
 Db |||||
 QY 238 CAAGGCAACGATCAGTAGTGGTCTGAGAGGACGACCGACCACTGGGACTGAGACACG 297
 Db |||||
 QY 316 GCCCAGACTCTACGGGAGGACGAGTGGGGAATTTTCGACAAATGGGGAAGCGCTGATC 375
 Db |||||
 QY 298 GCCCAGACTCTACGGGAGGACGAGTGGGGAATTTTCGACAAATGGGGAAGCGCTGATC 357
 Db |||||
 QY 376 CAGCAATCCCGGTGAGTGAAGAAGG-CTTCGGGTGTGAAAGCTCTTTTCAGTTCGAGAAGA 434
 Db |||||
 QY 358 CAGCAATCCCGGTGAGTGAAGAAGGCTTCCGGTGTGAGAGCTCTTTTAGTCAGANAAGA 417
 Db |||||
 QY 435 AAAGTGTGTGACTAATAATCAACTTATGATGGTACCGACAGAGAAGACGACCGGCTAAC 494
 Db |||||
 QY 418 AAGAATCATGATGAATAATATGATTATGACGGTACTGACAGAAAAAAGCAGCGGCTAAC 477
 Db |||||

Qy	495	TACGTGCCAGCAGCCGCGTAAATCGTTAGGTTGCAAGCGTTTAATCGGAATTACTGGGCGT	554
Db	478	TACGTGCCAGCAGCAGCCGCGTAAATCGTAGGGTCGAGCGTTAATCGGAATTACTGGGCGT	537
Qy	555	AAAGGGTCGCGAGCGCGCTTCTAGTCAGATGTGAAATCCCGCGGCTTTAACTCGGGAAT	614
Db	538	AAAGGGTCGCGAGCGCGGTTTTGTAGTCAGATGTGAAAGCCCGCGGCTTTAACTCGGGAAT	597
Qy	615	TGCGTTTGAAACTACAAAGCTAGAGTGTAGCAGAGGGGGTGGAAATTCATGTGTAGCAG	674
Db	598	TGCGTTTGAAACTTCAAGGCTAGAGTGCAGCAGAGGGGAGTGGAAATTCATGTGTAGCAG	657
Qy	675	TGAAATCGGTAGAGATATGGAGAACATCGATGGCGAAGCAGCCCTGGGTGTTAACTACT	734
Db	658	TGAAATCGGTAGAGATGTGGAGAAACACCGATGGCGAAGCAGCTCCCTGGGTGTTGACACT	717
Qy	735	GACGCTCATGTGCACAAAGCGTGGGGAGCAAAACAGGATTAGATACCTCGTGTAGTCCACGCC	794
Db	718	GACGCTCATGCACGAAGCGTGGGGAGCAAAACAGGATTAGATACCTCGTGTAGTCCACGCC	777
Qy	795	CTAAACGATGTCAACTAGTTGTTGGGCCCTTACTA--GGCTTGGTAACGTAGCTTACGCCGT	852
Db	778	CTAAACGATGTCAACTGGTTGTCCGATCTAAATTAAGGATTTGGTAACGTAGCTTACGCCGT	837
Qy	853	GAAGTTTGACCGCCTGGGGAGTACGGTCGACGAGATTAAAACTCAAAGGAATTGACGGGGAC	912
Db	838	GAAGTTTGAACGCCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGGAATTGACGGGGAC	897
Qy	913	CCGCAAAAGCGGTGGATTTATGTGGATTAATTCGATCGAACCGGAAAAAAGCTTACCTACCC	972
Db	898	CCGCAAAAGCGGTGGATTTATGTGGATTAATTCGATGCAACGGGAAAAAAGCTTACCTACCC	957
Qy	973	TTGACATGTAGCGAAATATTTTAGAGATAAAATAGTGCC--TTCCGGAAACGCTAACACAGG	1030
Db	958	TTGACATGCTTGGAAATCTAGTGGAGACATTAAGAGTGCCTGAAGGGAGCCAAAGACACAGG	1017
Qy	1031	TGCTGCATGCGTGTGFCGACGCTCGTGTGAGAGATGTGGGTTAAGTCCCGCAACAGAGCG	1090
Db	1018	TGCTGCATGCGTGTGFCGACGCTCGTGTGAGAGATGTGGGTTAAGTCCCGCAACAGAGCG	1077
Qy	1091	CAACCTTGTTCANTTAATGCCCATCATTTAGTTTGGGCACCTTAATAGAGACTGCGCGTGAC	1149
Db	1078	CAACCTTGTTCACATAATGTGTATCATTTCTAAATGAGCACATTTAGTGGAGCTGCGGTGAC	1137
Qy	1150	AAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGCGCCCTTATGGGTAGGGCTTCAC	1209
Db	1138	AAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGCGCCCTTATGGGTAGGGCTTCAC	1197
Qy	1210	ACGTAAATCAANTGGCGGTGACAGGGGTTCCCAACCCGCGAGGGGGAGCTTAATCTCAGAA	1269
Db	1198	ACGTAAATCAANTGGCGGTGACAGAGGGTTGCCAAACCCGCGAGGGGGAGCCAACTCAGAA	1257
Qy	1270	AGCGGTGCTAGTCCGGATCGGAGTCTGCAACTCGACTCCGTGAAGTCGGAATCGCTAGT	1329
Db	1258	AGCACGTGCTAGTCCGGATCGGAGTCTGCAACTCGACTCCGTGAAGTCGGAATCGCTAGT	1317
Qy	1330	AATCGCGGATCAGCATGTGCGGTGGAATACGTTCCCGGGTCTTGATACACACGCCCGTCA	1389
Db	1318	AATCGCGGATCAGCATGCGCGGTGGAATACGTTCCCGGGTCTTGATACACACGCCCGTCA	1377
Qy	1390	CACCATGGGAGTGGTTTTACCAAGAAGCAGATAGTCTTAAACCGTAA--GAGGGCGTTTGCCA	1448
Db	1378	CACCATGGGAGTGGTTTTACCAAGAAGCAGATAGTCTTAAACCGTAAAGGAGACGCTTGCCA	1437
Qy	1449	CGGCGAGATTCACTAGG	1467
Db	1438	CGGTGGGGTCACTAGCTGG	1456

RESULT 11
ADM32707
.ID ADM3

[illegible]

RESULT 11
ADM32707
.ID ADM3

[illegible]

Db	1381	CACGCCCGCTCACACCATGGAGTGGGTTTCCACGAGAAGTAGGTAGCTTAACCTTCGGGA	144
Qy	1437	GGCGTTTCCACGGCGAGATTCATGACTGG	1467
Db	1441	GGCGCTTACCACGGTGAGATTCATGACTGG	1471
RESULT 13			
ID	AAC86030 standard; cDNA; 1485 BP.		
XX	AAC86030;		
XX	11-SEP-2003 (revised)		
DT	29-AUG-2001 (first entry)		
XX	16S rDNA, ProPel.		
XX	16S rDNA; polyphosphate accumulating organism; PAO; probe; primer;		
KW	detection; phosphorus; waste water; sludge; ss.		
XX	Propionivibrio pelophilus.		
XX	WO200146459-A1.		
XX	28-JUN-2001.		
XX	28-DEC-2000; 2000WO-AU001611.		
PF	23-DEC-1999; 99AU-00004867.		
XX	(CRCW-) CRC WASTE MANAGEMENT & POLLUTION CONTROL.		
PA	Hugenholtz P, Crocetti GR, Tyson GW, Blackall LL;		
PI	WPI; 2001-408656/43.		
DR	Novel oligonucleotide probe or primer useful for detecting polyphosphate		
PT	accumulating organism in a sample, comprises a sequence that is unique to		
PT	16S rDNA of polyphosphate accumulating organisms.		
XX	Claim 4; Fig 3; 54pp; English.		
XX	The sequences given in AAC86021-30 represent 16S rDNA sequences from		
CC	polyphosphate accumulating organisms (PAOs). Sequences which are unique		
CC	to these 16S rDNA sequences are used to create a probe or primer for		
CC	detecting the relevant organisms. The primer/probe sequences are useful		
CC	for detecting PAO cells in a sample, by treating cells in the sample to		
CC	fix cellular contents, contacting fixed cells with the primer/probe which		
CC	is labelled with a radiolabel, a reporter group or a hapten, under		
CC	conditions which allow the probe to hybridize with 16S rDNA within the		
CC	fixed cell, removing unhybridized probe from the fixed cells, and		
CC	detecting the labeled probe-RNA hybrid by fluorescence in situ		
CC	hybridization. The primer/probe sequences are useful for identifying PAOs		
CC	that are capable of biologically removing phosphorus from waste water.		
CC	Rapid assessment of the presence of a number of PAOs in a waste water		
CC	sample, can be done using the primer/probe sequences. They allow quick		
CC	and convenient assessment of whether a sludge or waste water sample		
CC	includes PAOs and allows quantitation of PAO cells in samples. (Updated		
CC	on 11-SEP-2003 to standardise OS field)		
XX	Sequence 1485 BP; 367 A; 482 G; 295 T; 0 U; 0 Other;		
XX	Query Match 81.0%; Score 1189; DB 4; Length 1485;		
XX	Beat Local Similarity 90.0%; Pred. No. 0;		
XX	Matches 1319; Conservative 0; Mismatches 140; Indels 6; Gaps 4		
Qy	9	GGCTCAGATTGAACCGCTGGCGCATGCTTTTACATGCAAGTCGAA CGGCAGACCGGTG	68
Db	1	GGCTCAGATTGAACCGCTGGCGCATGCTTTACATGCAAGTCGAA CGGCAGATGGGTG	60
Qy	69	CTTGCACTGTGGCGAGTGGCGGACGGTGAGTAATGCATCGGAACGTGTCACAAGTG	128

CC includes PAOs and allows quantitation of PAO cells in samples. (Updated
 CC on 06-AUG-2003 to correct OS field.)

XX Query Match 79.8%; Score 1171.2; DB 4; Length 1460;
 Best Local Similarity 90.0%; Pred. No. 0;
 Matches 1312; Conservative 0; Mismatches 138; Indels 8; Gaps 5;

QY	16	ATTGAAACGCTGGCGGCACTGCTTTACACATCGAAGTCGAACGGCAGCAGCGGTGCTTGCAC	75
DB	1	ATTAAACGCTGGCGGCACTGCTTTACACATCGAAGTCGAACGGCAGCAGCGGTGCTTGCAC	58
QY	76	CTGGTGGCGAGTGGCGGACGCGGTGAGTAATGCAATCGGAACGTGTCCAGAAAGTGGGGATA	135
DB	59	CTGGTGGCGAGTGGCGGACGCGGTGAGTAATGCAATCGGAACGTGTCCAGAAAGTGGGGATA	118
QY	136	ACGCATCGAAAGATGTGCTTAATACCGCATATTTCTACGGAAGNAAGCAGGGATCGAAA	195
DB	119	ACGCAGCGAAAGCTACGCTAATACCGCATATTTCTGAGCAGGAAGCAGGGATCGCAA	178
QY	196	GACCTTGTGCTTTTGGAGCGGCCGATCCCTGATTAGCTAGTTGGTGGGTAAAGGCCCTAC	255
DB	179	GACCTTGTGCTTTTGGAGCGGCCGATGTGCAATAGCTAGTTGGTGGGTAAAGGCCCTAC	238
QY	256	CAAGGCAACGATCAATAGTTGGTCTGAGAGGACGACAGCCACACTGGGACTGAGACACG	315
DB	239	CAAGGCAACGATCAATAGTTGGTCTGAGAGGATGATCCGACACTGGGACTGAGACACG	298
QY	316	GCCAGACTCTACGGAGGACGAGTGGGGAAATTTTGGCAATGGCGGAAAGCCTGATC	375
DB	299	GCCAGACTCTCTACGGAGGACGAGTGGGGAAATTTTGGCAATGGCGGAAAGCCTGATC	358
QY	376	CAGCAATGCCGCTGAGTGAAGAAAGG-CTTCCGGTGTGTAAGCTCTTTTCAGTTCGAGAAGA	434
DB	359	CAGCAATGCCGCTGAGTGAAGAAAGGCTTCGGTGTGTAAGCTCTTTTCGGCGGGAAGA	418
QY	435	AAAGGTTGTGATAATATCAACTTAATGATGTAACGACAGAAAGACACCGGCTAAC	494
DB	419	AATGCTTGGGTTAATACCTTGAGTAGACGCTACCGGATTAAGAAAGCAGCAGCGGCTAAC	478
QY	495	TACGTGCCAGCAGCGCGGTAAATACGTAGGTTGCAAGCGTTAAATCGGAAATTTACTTGGCGGT	554
DB	479	TACGTGCCAGCAGCGCGGTAAATACGTAGGTTGCAAGCGTTAAATCGGAAATTTACTTGGCGGT	538
QY	555	AAAGGTTGCCAGCGCGCTTTGTAAGTCAGATGTGAATATCCCGGCTTAACTCTGGGAAT	614
DB	539	AAAGGTTGCCAGCGCGCTTTGTAAGTCAGATGTGAATATCCCGGCTTAACTCTGGGAAT	598
QY	615	TGCGTTTGAAACTACAAAGCTAGATGTAGCAGAGGGGGTGGAAATTCATGTGTAGCAG	674
DB	599	TGCATTTGAGACTGCAAGACTGGAGTTTGGCAGAGGGGGTGGAAATTCACGTGTAGCGAG	658
QY	675	TGAAATGCTAGATATGGAAGAACATCGATGGCGAAGGCGAGCCCTCGGTTAAACACT	734
DB	659	TGAAATGCTAGATATGGAAGAACACCGATGGCGAAGGCGAGCCCTCGGTTAACTACT	718
QY	735	GACGCTCATGCAAGAAAGCGTGGGAGCAAAACAGGATTTAGATACCTTGGTGTAGTCCAGCC	794
DB	719	GACGCTCATGCAAGAAAGCGTGGGAGCAAAACAGGATTTAGATACCTTGGTGTAGTCCAGCC	778
QY	795	CTAAACGATGCAACTAGTTGTGG--GCCCTTACTAGCTTGGTAAACGTAGCTAACCGGT	852
DB	779	CTAAACGATGCAACTAGTTGTGGAGGGGTAAACCTTTTAGTGCCTAGCTAACCGGT	838
QY	853	GAAGTGTGACCGCTCGGGAGTACGCTCGCAGGATTTAAACCTCAAGAGGAATTTGACGGGAC	912
DB	839	GAAGTGTGACCGCTCGGGAGTACGCGCCGCAAGGCTTAAACCTCAAGAGGAATTTGACGGGAC	898
QY	913	CGCACAAGCGGTGGATTATGTGGAATTAATTCGATGCAACGCGCAAAAACCTTACTACCC	972
DB	899	CGCACAAGCGGTGGATTATGTGGAATTAATTCGATGCAACGCGCAAAAACCTTACTACCC	958

RESULT 15

AD45500	ID	ADR45500 standard; DNA; 1530 BP.
XX	AC	ADR45500;
XX	DT	18-NOV-2004 (first entry)
XX	DE	16S rRNA gene 357f-518r region DNA fragment SeqID89.
XX	KW	357f-518r; 16S rRNA; beta proteobacterium; ammonia oxidising bacteria;
XX	KW	activated sludge; ammonia liquid treatment plant; chemical oxygen demand;
XX	KW	COD; reduction; nitrification; denitrifying; ds.
XX	OS	Unidentified.
XX	PN	JP2004242578-A.
XX	PD	02-SEP-2004.
XX	PF	13-FEB-2003; 2003JP-00035713.
XX	PR	13-FEB-2003; 2003JP-00035713.
XX	PA	(YAWA) NIPPON STEEL CORP.
XX	DR	WPI; 2004-620179/60.
XX	PT	Novel DNA fragment of microorganisms existing in activated sludge of
XX	PT	ammonia liquid treatment plant, useful as index microorganisms for
XX	PT	evaluating nitrification or denitrifying capability of ammonia liquid.
XX	PS	Claim 45; SEQ ID NO 89; 133pp; Japanese.
XX	CC	This invention relates to a novel DNA fragment comprising the 357f-518r
CC	CC	region of the 16S rRNA gene of beta proteobacteria, belonging to the

CC ammonia oxidising bacteria group, or CFB Bacteroides where bacteria
 CC exists in activated sludge of an ammonia liquid treatment plant and used
 CC for chemical oxygen demand (COD) reduction. The invention is useful in
 CC the identification of microorganisms as nitrification or denitrifying
 CC index microorganisms for evaluating the nitrification or denitrifying
 CC capability of ammonia liquid of the activated sludge by fluorescence in
 CC situ hybridisation (FISH). The invention is also useful for developing
 CC apparatus for the processing of ammonia liquid. The DNA fragment enables
 CC evaluation of the nitrification or denitrifying capability of
 CC microorganisms. The present sequence is that of a 16S rRNA gene 357f-518r
 CC region of the invention.

XX Sequence 1530 BP; 406 A; 337 C; 474 G; 313 T; 0 U; 0 Other;

Query Match 79.8%; Score 1170.2; DB 13; Length 1530;
 Best Local Similarity 91.6%; Pred. No. 0;
 Matches 1350; Conservative 0; Mismatches 108; Indels 15; Gaps 10;

Qy	5	TCATGGCTCAGATTGAACGCTGGCGGCATGCTTTACATGCAAGTCGAACGGCAGCACG	64
Db	9	TCCTGGCTCAGATTGAACGC-GGCGGCATGCTTTACATGCAAGTCGAACGGCAG--CG	65
Qy	65	GGTGTTCACCTGGTGGCGAGTGGCGGACGGGTGAGTAATGCAATCGGAACGTGTCCAGA	124
Db	66	GGGGCTTAGGCTGGCGGCGAGTGGCGAAGCGGTGAGTAATACATCGGAACGTGTCCCTTA	125
Qy	125	AGTGGGGATACCGCATCGAAGATGCTTAATACCGCATATTTCTACGAGGAGGAACGA-184	184
Db	126	AGTGGGGAATACCGCATCGAAGATGCTTAATACCGCATAT-TCTCTCAGGAGGAAGCA	184
Qy	185	GGGATCGAAGACCTTGCTTTGGAGCGCGCATGCTTATGATGAGTGTGTTGGGG	244
Db	185	GGGATCGAAGACCTTGCTTTGGAGCGCGCATGCTTATGATGAGTGTGTTGGGG	244
Qy	245	TAAAGGCTTACCAAGCAACAGTCACTAGTGTGCTGAGAGGACGACCACTGGG	304
Db	245	TAAAGGCTTACCAAGCAACAGTCACTAGTGTGCTGAGAGGACGATCAGCCACTGGG	304
Qy	305	ACTGAGACAGCGCCAGACTCTCTACGGAGGAGCAGTGGGGAAATTTGGACAAATGGGCG	364
Db	305	ACTGAGACAGCGCCAGACTCTCTACGGAGGAGCAGTGGGGAAATTTGGACAAATGGGCG	364
Qy	365	AAAGCTGATCCAGCAATGCGCGTGTGAGTGAAGAGGCTTCGGGTGTAAAGCTCTTTCA	424
Db	365	AAAGCTGATCCAGCAATGCGCGTGTGAGTGAAGAGGCTTCGGGTGTAAAGCTCTTTTA	424
Qy	425	GTCGAGAGAAAGGTTGTGACTAATAATCAAACTATGATGTCGACGACGAGGAAGC	484
Db	425	GTTGGAAGAAAGATTTATGTTAATACTATATTTATGACGTACCAACAGAAAGC	484
Qy	485	ACCGGCTAATCTGTCGAGCAGCGCGGTAAATAGTAGGTGCAAGCGTTAATCGGAAT	544
Db	485	ACCGGCTAATCTGTCGAGCAGCGCGGTAAATAGTAGGTGCGAGCGTTAATCGGAAT	544
Qy	545	TACTGGGGTAAAGGGTGGCGAGCGGCTTTGTAAGTCAGATGTAATCCCGGGCTTA	604
Db	545	TACTGGGGTAAAGGGTGGCGAGCGGCTTTGTAAGTCAGATGTAATCCCGGGCTTA	604
Qy	605	ACCTGGGAATTTGCGTTTGAAGTCAAAAGCTAGAGTGTAGCAGAGGGGGGTGGAATCCA	664
Db	605	ACCTGGGAATTTGCGTTTGAAGTCAAAAGCTAGAGTGTAGCAGAGGGGGGTGGAATCCA	664
Qy	665	TGTGTAGCAGTGAATGCGTAGAGATATGGAAGAAATCGATGGCGAAGGCGCCCTG	724
Db	665	TGTGTAGCAGTGAATGCGTAGAGATATGGAAGAAATCGATGGCGAAGGCGCCCTG	724
Qy	725	GTTTAAGTCACTGACGCTCATGACGAAAGCGTGGGAGCAACAGGATTTAGATACCTGGT	784
Db	725	GTTTGAACACTGACGCTCATGACGAAAGCGTGGGAGCAACAGGATTTAGATACCTGGT	784
Qy	785	AGTCCAGCCCTAAACGATGTCAACTAGTGTGGGCTTACTA--GGCTTTGGTAAACGTA	842
Db	785	AGTCCAGCCCTAAACGATGTCAACTAGTGTGGGCTTACTA--GGCTTTGGTAAACGTA	842

Qy	843	GCTAACCGGTGAAGTTGACCGCTGGGAGTACGGTCCGAGATTAATAACTCAAGGAAT	902
Db	845	GCTAACCGGTGAAGTTGACCGCTGGGAGTACGGTCCGAGATTAATAACTCAAGGAAT	904
Qy	903	TGACGGGAGCCCGCACAGCGGTGGAATTTATGTGGATTAATTCGATGCAACGCAAAAACC	962
Db	905	TGACGGGAGCCCGCACAGCGGTGGAATTTATGTGGATTAATTCGATGCAACGCAAAAACC	964
Qy	963	TTACCTACCTTTGACATGACGGAATATTTTAGAGATTAATAATAGTGCC--TTGCGGAACG	1020
Db	965	TTACCTACCTTTGACATGACGGAATCTAATGGAGACATAAGAGTGCCCGTAAGGAAACC	1024
Qy	1021	CTAACACAGGTGCTGCATGGC--TGTGCTGACGTGCTGCGAGATGTTGGGTTAAGTCC	1079
Db	1025	GGGACACAGGTGCTGCATGGGCTGTCGTCAGCTCGTGTGAGATGTTGGGTTAAGTCC	1084
Qy	1080	CGCAACGA--GCGCAACCTTTGATTAATTTGTCAT--CATTTAGTTGGGCACTTTAATG	1135
Db	1085	CGCAACGAGCGCAACCTTTGTCGTTAAATTTGCTATCCATTTAATGACCACTTTAAGC	1144
Qy	1136	AGACTGCGGTGACAAACCGGAGAAAGGTGGGATGACGTCAAGTCTCATGGCCCTTAT	1195
Db	1145	AGACTGCGGTGACAAACCGGAGAAAGGTGGGATGACGTCA--AGTCTCTCATGGCCCTTAT	1203
Qy	1196	GGGTAGGGCTTTCACAGTAAATACAAATGCGCGGTACAGAGGCTTGCACACCGCGAGGGG	1255
Db	1204	GGGTAGGGCTTTCACAGTAAATACAAATGCGCGGTACAGAGGCTTGCACATCCGCGAGGG	1263
Qy	1256	AGCTAAATCTCAGAAAGCGCGTGTAGTCCGGATCGGAGTCTGCAACTGCACTCCGTGAAG	1315
Db	1264	AGCCAAATCTCAGAAAGCGCGTGTAGTCCGGATCGGAGTCTGCAACTGCACTCCGTGAAG	1323
Qy	1316	TCGGAATGCGTGTAGTAAATCGCGGATCAGCATGTGCGCGTGAATACTTCCCGGCTTCTGA	1375
Db	1324	TCGGAATGCGTGTAGTAAATCGCGGATCAGCATGTGCGCGTGAATACTTCCCGGCTTCTGA	1383
Qy	1376	CACACCGCGCTTCACACATGGGAGTGGGTTTACCAGAGCAGATAGTCTAACCGTAA--	1434
Db	1384	CACACCGCGCTTCACACATGGGAGTGGGTTTACCAGAGCAGATAGTCTAACCGTAA--	1443
Qy	1435	GAGGGCGTTTGCACACGCGGAGATTTCATGACTGG	1467
Db	1444	GAGGGCGTTTGCACACGCGGAGATTTCATGACTGG	1476

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 Job time : 940 secs

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